

Tue May '15 08:41:17 2001

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OM protein - protein search, using sw model
Run on: May 14, 2001, 17:32:48 ; Search time 45.24 Seconds
(without alignments)
731,598 Million cell updates/sec

US-09-254-590-19.rag

Title: US-09-254-590-19
Sequence: 2954
Scoring table: 1 MSSCRINGCMRPLSNLSAS.....SSRRSSSTAPPTSSSS 579
Searched: Gapop 10.0, Gapext 0.5
Total number of hits satisfying chosen parameters: 390729
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries

Database :
1: /SID56/gcgdata/geneseq/geneseq/AA1980.DAT.*
2: /SID56/gcgdata/geneseq/geneseq/AA1981.DAT.*
3: /SID56/gcgdata/geneseq/geneseq/AA1982.DAT.*
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21: /SID56/gcgdata/geneseq/geneseq/AA2000.DAT.*
22: /SID56/gcgdata/geneseq/geneseq/AA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

	Score	Query Match	Length	ID	Description
2	2954	100.0	579	19	Human hSK2 protein
3	2881.5	97.5	580	19	Human hSK2 protein
4	2123.5	72.0	557	19	Human hSK2 protein
5	2123.5	72.0	557	19	Human hSK2 protein
6	2121.5	72.0	557	19	Human hSK2 protein
7	2113.5	71.8	736	19	Human hSK2 protein
8	2057.13	71.5	731	20	Human hSK2 protein
9	1868.5	69.7	731	20	Human hSK2 protein
10	1752.5	63.3	731	20	Human hSK2 protein
11	964.5	59.3	458	19	Human hSK2 protein
	32.7		217	20	Human hSK2 protein

RESULT	ID	ALIGNMENTS
1	W63707	01-OCT-1998 (first entry)
2	W63707	Small conductance calcium-activated potassium channel protein 2;
3	W63707	W09811139-A1.
4	W63707	19-MAR-1998.
5	W63707	10-SEP-1997.
6	W63707	17-APR-1997.
7	W63707	11-SEP-1996.
8	W63707	07-MAR-1997.
9	W63707	97US-0045233.
10	W63707	96US-0026451.
11	W63707	97US-0040052.
12	W63707	(ICAG-) ICAGEN INC.
13	W63707	(UYOR-) UNIV OREGON HEALTH SCI.
14	W63707	Adelman JP, Bond CT, Maylie J, Silvia CP.
15	W63707	WPI: 1998-207332/18.
16	W63707	N-Psdb: V35457.
17	W63707	DNA encoding calcium-activated potassium channel - useful in assays

...+15y compounds which are
...100: English

	AC	XX	63702; (first entry)
	AD	XX	01-OCT-1998
	AE	XX	Rat rSK2 protein.
	AF	XX	Small conductance calcium-activated potassium ion flux.
	AG	XX	rSK2; rat; potassium ion flux.
	AH	XX	Rattus sp.
	AI	XX	WO981139-A1.
	AJ	XX	WO981139-A1.
	AK	XX	19-MAR-1998.
	AL	XX	97WO-US16033.
	AM	XX	10-SEP-1997;
	AN	XX	97US-0045233.
	AO	XX	17-APR-1997;
	AP	XX	96US-0026451.
	AQ	XX	11-SEP-1996;
	AR	XX	97US-0040052.
	AS	XX	07-MAR-1997;
	AT	XX	(ICAGEN) ICAGEN INC. HEALTH SCT.
	AV	XX	(UYOR-) UNIV OREGON
	AW	XX	MAYLIE J, SILVA CP;
	AX	XX	Adelman JP, Bond CT,
	AY	XX	Pfizer Inc., New York, NY
	AZ	XX	WPI: 1998-207332/18.
	B1	XX	N-PDB: V35446.
	B2	XX	DNA encoding calcium-activated potassium channel - useful in assays
	B3	XX	to identify compounds which increase or decrease potassium ion flux
	B4	XX	claim 2: page 94-95: 15pp. English.
	B5	XX	of the rat small conductance calcium-activated potassium channel where
	B6	XX	the weight of between 40 and 60 ps and the weight of between 40 and 60 ps
	B7	XX	when the weight of between 40 and 60 ps and the weight of between 40 and 60 ps
	B8	XX	when the weight of between 40 and 60 ps and the weight of between 40 and 60 ps
	B9	XX	when the weight of between 40 and 60 ps and the weight of between 40 and 60 ps
	BA	XX	when the weight of between 40 and 60 ps and the weight of between 40 and 60 ps
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	BD	XX	when the weight of between 40 and 60 ps and the weight of between 40 and 60 ps
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	BH	XX	when the weight of between 40 and 60 ps and the weight of between 40 and 60 ps
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	BL	XX	when the weight of between 40 and 60 ps and the weight of between 40 and 60 ps
	BM	XX	when the weight of between 40 and 60 ps and the weight of between 40 and 60 ps
	BN	XX	when the weight of between 40 and 60 ps and the weight of between 40 and 60 ps
	BO	XX	when the weight of between 40 and 60 ps and the weight of between 40 and 60 ps
	BP	XX	when the weight of between 40 and 60 ps and the weight of between 40 and 60 ps
	BQ	XX	when the weight of between 40 and 60 ps and the weight of between 40 and 60 ps
	BR	XX	when the weight of between 40 and 60 ps and the weight of between 40 and 60 ps
	BS	XX	when the weight of between 40 and 60 ps and the weight of between 40 and 60 ps
	BT	XX	when the weight of between 40 and 60 ps and the weight of between 40 and 60 ps
	BU	XX	when the weight of between 40 and 60 ps and the weight of between 40 and 60 ps
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	BX	XX	when the weight of between 40 and 60 ps and the weight of between 40 and 60 ps
	BY	XX	when the weight of between 40 and 60 ps and the weight of between 40 and 60 ps
	BZ	XX	when the weight of between 40 and 60 ps and the weight of between 40 and 60 ps
	C1	XX	when the weight of between 40 and 60 ps and the weight of between 40 and 60 ps
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	CT	XX	when the weight of between 40 and 60 ps and the weight of between 40 and 60 ps
	CU	XX	when the weight of between 40 and

[illegible][illegible]

CC probes specific for the DNA can be used to detect the presence of the
CC protein or DNA sequences in a sample. Host cells expression of the
CC protein can be used in assays to identify compounds which increase or
CC decrease the potassium ion flux through the protein. The transfected host
CC cell can also be used for the recombinant production of the protein. The
CC DNA sequences can also be used for determine mutations in the SK and IK
CC genes in a computer system. The proteins encoded by the SK and IK genes
CC can be used in a computer system for determining their three dimensional
CC structure, which is useful for determining ligands that bind to the
CC proteins.
XX
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XX Sequence 557 AA;

Query Match	72.08;	Score 2125.5;	DB 19;	Length 557;
Best Local Similarity	73.28;	Pred NO 6 6e-193.		

Matches 428; Conservative 48; Mismatches 72; Indels 37; Gaps 4.

QY 1 MSSCRRYNGCVMRPLSLNLASRRNLHENDSEAOPIQPPASVGGGGCASSPSAAAAAAAAVS 60
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Db 1 mssckysgcmkplslrslasrrnliaetegqplq-----lfp----- 39

61 SSAPEIVSKPEHHNSNNLALYGTGG-----GGSTGGGGGGGGSSGHGSSSGTKSSKKKN 114

20 40 suppressorlesscunninglyclimbercunningagclca-----sstclpkanrkkn 89

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Db      150 s|stl||q||i|av|htreva|fv|idnca|ddr|i|am|tver|l|v|is|em|wca|ib|ncor|k    308
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QY 235 FTWTARLAFSYAPSTTTADVDIILSIPEFLRLYL IARVMLHSKLFTDASSRSIGAI NKI 294

Db 210 ffwrtarlafsytpsræadvdiilsipmflrlyiarvmlhsklftdassrslgalnki 269

295 NFNTREVMKTLMTICPGTVLLVESISLWIAAWTVRACERYHDQDVTSNFLGAMWLISI 354

270 mmlclvmlclcpqvlvisislwlaawtvrceryhdqdvtsnflgamwlisi 329

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QY 475 QANTLVDLAKTQNMIDMISDLNERSSEDEFEKRIVTLETKEETLIGSIHALPGLISOTIRO 534

Db 450 gantlvdiskmqnvydilitelndrsedlekqigslesklehtasfnsplliadtirg 509

QY 535 QQRDFIEAQMESYDKHVITYNAERSRSSRRRRSSSTAPPTSSESS 579

[illegible]

RESULT 4

ID	standard; 736 AA.
W63717	Protein; 736 AA.

AC
XX
W03/L/;

XX

conductance of the system is

XX
AM
115A3, 11411A11 10H 1110X.

OS Homo sapiens.

Tue May '15 08:41:17 2001

us-09-254-590-19.rag

Page 5

sq	Sequence	732 AA
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Query Match	71.8%;	Score 2121.5;	DB 19;	Length 732;
Best Local Similarity	72.8%;	Pred. No. 2,46-192;		
Matches 426;	Conservative 49;	Mismatches 73;	Indels 37;	Gaps 4

QY		1	MSGSGVGVNHRPLSNLSASRRLHMDSEKOPLOPPAVSGGGGASSPFAAAAAAANAAYS	60
Db		176	mssckysggvmxpriptsrastrnmlleaepegprfq-----lsp-----	214
QY		61	SSAEIYVSKPPEHNNSNNLLALVTGTG-----GGSTGGGGGGGSGHGSSGTRKSCKKN	114
Db		215	snpellilsredhnahqllhmpnathqhagta-----gstffpkakrh	264
QY		115	ONIGYLGRRARLEFKERRKRSIDVALIFGEGIVVMVEPELWSGAYDKASLYSLAKCDI	174
Db		265	qdlygklghrralfekrkrisdvallylgmrlgvmmvletelswglvsdmsftalkcll	324
QY		175	SISTILLGLIYYAHAREIQLEFWDVNGADWRIAMTYERIFICTELLYCAIHPIRGNTY	234
Db		325	sistlllglllyshrevgfvdmgadawrlamtyerillylslemlycalhpipegk	384
QY		235	FHWTAFLAFSAFTTADVDIIISIPMFRLYLARVMLHSKLFTPDASSRIGALNKI	294
Db		385	fhwtaflafsfytsreaadvallispmfirlylarwmllhsklftdassrsigalnki	444
QY		295	NFWTFVAKTLMTICGETVLVFSISMWITAAWTYACAEERYHOODVTSNFPGAMWLISI	354
Db		445	nfwtfvkmktlmctpcgtvlmfstislwiilaavtvceryhoogdvtsnfpgamwlisi	504
QY		355	TPLSICGYDMVPNYCGKGVCILFTGMAGCTALVVAVVARKLELTAKRYHANMDDQ	414
Db		505	tplsicgydmvpnycgkgvcilftgmagctalvvavvarkeltakehyhnmddtg	564
QY		415	LTKRVNAANVLEETWLYKNTLYKKTDIAHAVVRKHOKRFLOAIHQLRYSKMEQRKND	474
Db		565	ltkrvnaanvlewtalykhkllkkidhakvrkhokrfqlgaqhqlrgvkmeqrksld	624
QY		475	QANTIVDLAKTONIMYMISDNLNERSDEFEKRIVLETKEFLTGSHALFGILSOTIRO	534
Db		625	qantivdlaskmgnwydfitelndrsedlekqjsleskltelhtastinsplliaclirg	684
QY		535	QQKDFIEAQMESYDKHYTVNAEKRSSSRSSRRSSSTAPPTSESS	579
Db		685	qqqdfllaivearigstavgtshapsdsipjistsfpptyss	729
RESULT		6		
W96312				
ID			W96312 standard; Protein; 731 AA.	
XX				
AC				
XX				
W96312:				
DT				
XX				
28-JUN-1999	(first entry)			
DE				
XX				
Human small conductance calcium activated potassium channel protein.				
OS				
Homo sapiens.				
PN				
WO99031889-A1.				
XX				
28-JAN-1999.				
PD				
XX				
PF				
14-JUL-1998:	98MO-US14902.			
XX				
PR				
08-JAN-1998:	98US-0070741.			

PR 15-JUL-1997; 97US-0052556.
 XX
 PA (REGC) UNIV CALIFORNIA.
 PI
 PI Chandy KG, Fantino E, Gargus JI, Gutman G, Kalman K;
 DR WPI: 1999-132165/11.
 DR N-PSDB; X08414.
 XX
 PR New human small conductance calcium activated potassium channel-3 -
 PI useful for diagnosis, treatment and prevention of particularly
 PI schizophrenia and bipolar disorders
 XX
 PS Claim 1; Fig 5; 95pp; English.
 XX
 CC Disorders associated with a dysfunctional or altered small
 CC conductance calcium-activated potassium channel-3 (hKCa3/KCNN3)
 CC comprise neuropsychiatric, neurological, neuromuscular and
 CC immunological disorders, specifically bipolar disease and
 CC schizophrenia. Transgenic animals comprising the hKCa3/KCNN3 gene
 CC as a transgene in their somatic and germ cell lines can be used
 CC as models for studying these conditions and their treatments.
 CC Antibodies (Ab) directed against the hKCa3/KCNN3 polypeptide
 CC or conservative variants of the polypeptide can be used to detect
 CC those at risk from these disorders and also in therapy against
 CC such disorders. Use of the wild type gene in gene therapy to treat
 CC these disorders is also contemplated.
 XX
 SQ Sequence 731 AA:

Query Match	71.5%	Score 2113.5	DB 20	Length 731
Best Local Similarity	73.6%	Pred. No. 14e-191		
Matches 426	Conservative 48	Mismatches 80	Indels 25	Gaps
Qy	1	MSSCRNGVWRPLSNLSARBNLEKMDSEAOPLQCPASVGGGGGASSPSAAAAA	60	
Db	175	msackysggyvnhkplsrtsarrnlleaetegpq-----lsp-----	213	
Qy	61	SSAPRYVSKPEHNHNSNLLAYGTGGGGSTGGGGGGGGGSHSSSSGKSSKKKNQIGK	120	
Db	214	snpeelvasredhahqclllhnp-----nathnqhagaasstlfpkankrnpisyn	269	
Qy	121	LGHRRLAEKKRRLSDVALLEGWFGIYVWVLETLISGWAYDASLYSLAKCLISLTI	180	
Db	270	lgntrapefkrtrlsdyallfgmfglyvwmvlelswlsqyskdsmtslakclisla	329	
Qy	181	LLGLIYVAREIQLEFWDVNGADWRIAMTVERIFCILEIIVCAIHPHPENYFETWTA	240	
Db	330	llglllayhltreaqlfvindgaddwrlamtyverillyislemlycalnmpjeyfficta	389	
Qy	241	LAESVASTTTADVDITLSIPMFLRLYLRLARVMLHSLKTLTDASRSISGALNKINPTR	300	
Db	390	lafsyprsedvdlislsplrtlyllarymlhsklffdasrsisgalnklnftrf	449	
Qy	301	VKTKLMTICGTVLLVFSISLMTIAATVYRACERHDOODVTSNPLGAWMLSTYFISIG	360	
Db	450	vmkfclmticpgtvllvflsislwiiaayracyerhqdqvtstflganmlstflsisg	509	
Qy	361	YCDWYPTTGYCKGVCLLTGIMGACSTLVAAVVAARKELTGAEKHVHNPMDTOLTKVK	420	
Db	510	ygdwvphlygkvqvcullgimgagcdalvaavarklrltkaekhyhnmfmmtqltkrik	569	
Qy	421	NAAAVLEFEMWLYKNTKLVKRKIDIAKVRKHQKFLQAIHOLRSVKEQKRLINDAANTV	480	
Db	570	naaanvlefwllykntklvkrkidiakvkrkhqkflqalhqdrsvkneqgklsdqantlv	629	
Qy	481	DLAKTIONMYMMSLDNERSGEDFEKRYLTLETFLTIGSIALHPLGLISOTITQOQRPI	540	
Db	630	dlakngvmydllelnrsedlektqysleskrehlntsfnsipjladrltvggqqql	689	
Qy	541	EAMQSYDKHTYNAERSSRSRRSSSTAPPPSSSS	579	

Tue May 15 08:41:17 2001

us-09-254-590-19.rag

Page 6

Db 690 salieargvavgtlthpisdplqvstsfcpvrtss 728

```
RESULT 7
W63703
ID W63703 standard; Protein: 553 AA.
AC W63703;
DE 01-OCT-1998 (first entry)
DE Truncated rat rsk3 protein.
DE
DE Small conductance calcium-activated potassium channel protein 3;
DE rsk3; rat; potassium ion flux.
DE
DE Rattus sp.
DE
DE W0981139-A1.
DE
DE 19-MAR-1998.
DE
DE 10-SEP-1997; 97WO-US16033.
DE
DE 17-APR-1997; 97US-0045233.
DE 11-SEP-1996; 96US-0026451.
DE 07-MAR-1997; 97US-0040052.
DE
DE (ICAG-) ICAGEN INC.
DE (UYOR-) UNIV OREGON HEALTH SCI.
DE
DE Adelman JP, Bond CT, Maylie J, Silvia CP;
DE WPI: 1998-207332/18.
DE N-PSDB: V35447.
DE
DE DNA encoding calcium-activated potassium channel - useful in assays
DE to identify compounds which increase or decrease potassium ion flux
DE
DE Claim 2; Page 96-97; 151pp; English.
DE
DE This sequence is the rat small conductance calcium-activated
DE potassium channel protein 3 (rsk3) of the invention. The proteins of the
DE invention are monomers of a calcium-activated potassium channel, where
DE the monomer: (1) has a calculated molecular weight of between 40 and
DE 80 kDa; and (11) has a unit conductance of between 2 and 60 pS when the
DE monomer is in the functional polymeric form of a potassium chain and is
DE expressed in a xenopus oocyte. Antibodies specific for the protein, and
DE probes specific for the DNA can be used to detect the presence of the
DE protein or DNA sequences in a sample. Host cells expression of the
DE protein can be used in assays to identify compounds which increase or
DE decrease the potassium ion flux through the protein. The transfected host
DE cell can also be used for the recombinant production of the protein. The
DE DNA sequences can also be used for determine mutations in the SK and IK
DE genes in a computer system. The proteins encoded by the SK and IK genes
DE can be used in a computer system for determining their three dimensional
DE structure, which is useful for determining ligands that bind to the
DE proteins.
DE
DE Sequence 553 AA:
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Query Match 71.5%; Score 2113; DB 19; Length 553;
Best Local Similarity 72.7%; Pred. No. 1e-191;
Matches 423; Conservative 49; Mismatches 60; Indels 50; Gaps 5;

```
QY 1 MSSCRNGVMPRLSNLSARNLHEMSEAPLOPPASVGGGAGSPPSAAAAAANAAS 60
DB 1 msackysggvmpslsrslasrrllleapegqplq-----lfsp----- 39
QY 61 SSAPEIWSKPEPHNNNSNNLALYCTG-----GGSTGGGGGGGGSSGSSCTSSKKKN 114
DB 40 snppellslsrchahqtlhhpntmhqhagta-----gstlfpkankrkx 89
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QY 115 ONIGYKLGHRRALFEKRRKRLSDYALIFMGCIYVWVITELISMGADYDKASLYSLAKCLI 174
DB 90 gniyqkklghrralfekrrkrlsdyalifmgciyvwvitelesmgadyskdselsakcli 149
QY 175 SLSTIILGLIYHARELOLPWNGADDMRLAMTYERIFICLEIYVCATHPITGNYT 234
DB 150 slstlilglilayharelolpwnagaddmrlamtyerificleilyvcathpitgny 209
QY 235 PTWTARLAESYAPSTTADVILISIPMFRLYLARMYLHSLKLTDDSSRSIGALNKI 294
DB 210 ftwtarlasysapsttadvilisiipmfrlylarmylhslkltddssrsigalnki 269
QY 295 NFNTREVMKTLMTICPGVILLVFSISLWITIAAMTVRACERYHDQDVTNSFGAMWLIIS 354
DB 270 nfntrevmktlmticpgvillvfsislwitiaamtvraceryhdqdvtnsfgamwliis 329
QY 355 TFLSTIGDMVPNTYCGKGVCLLTGIMAGCTALVVAVRKLEIYKAEKRVHFMMDIQ 414
DB 330 tflstigdmvntycgkgvclltgimagctalvvaavrkleiykaekrvhfmmdiq 389
QY 415 LTRRYKNAANVLRFTWLYKNTKLYKKIDAKYRKORRFLQAIHQLSYKKEORLND 474
DB 390 ltrryknaanvlfretwlykntklykkidakyrkorrfllqaihqlsykkeorlnd 449
QY 475 QANTLVDLAKTONIMTDMISDNERSDEFEKRIVTLETLETLGSIHALPGLISQITRQ 534
DB 450 qantlvdlaktonimtdmisdnersdefekrivtletletlsgihalpplisqitrq 509
QY 535 QQRDFIEAOMESYDKHVTYNAERSRSSRRSSRAAPPTSS 576
DB 510 qqqqllatavearglsav-----gsthappss 538
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RESULT 8
ID Y32018 standard; Protein: 731 AA.
AC Y32018;
DE 05-JAN-2000 (first entry)
DE
DE Human cation channel protein.
DE
DE Cation channel protein; CCP; ion transport; arrhythmia;
DE diabetes mellitus; seizure; asthma; hypertension; therapy;
DE protein engineering; human.
DE
DE Homo sapiens.
DE
DE Key Location/Qualifiers
DE Region 61..119 /note="crystal region"
DE
DE W09947923-A2.
DE
DE 23-SEP-1999.
DE
DE 22-MAR-1999; 99WO-US06307.
DE
DE 20-MAR-1998; 98US-0045529.
DE 02-APR-1998; 98US-0054347.
DE
DE (UYRQ ) UNIV ROCKEFELLER.
DE
DE Mackinnon R;
DE WPI: 1999-601131/51.
DE
DE Assays for screening compounds which interact with cation channel
DE proteins, useful for providing agents for treatment of diseases
DE
DE Claim 21; Page 148-150; 165pp; English.
```

us-09-254-590-19.1aa

Tue May 15 08:41:17 2001

XX The present sequence represents a human cation channel protein
 CC (CCP). The invention provides an assay for screening potential
 CC drugs or agents which interact with CCPs using prokaryotic CCPs
 CC (such as those given in Y32009-12) mutated, using recombinant DNA
 CC technology, to mimic the physiological function and chemical
 CC properties of a functional eukaryotic CCP (such as those given in
 CC Y32013-22). An example of a mutated prokaryotic CCP is given in
 CC Y32024. The crystal region of the CCP may also be used to treat
 CC assay. The drugs or agents obtained can be used, such as cardiac
 CC conditions related to the function of CCP in vivo, such as cardiac
 CC arrhythmia, diabetes mellitus, seizure disorder, asthma or
 CC hypertension. The invention has overcome the physical limitations
 CC regarding the isolation and purification of eukaryotic CCPs.

Sequence 731 AA:

Query Match 69.7%; Score 2057.5; DB 20; Length 731;
 Best Local Similarity 71.5%; Pred. No. 2,9e-186;
 Matches 418; Conservative 48; Mismatches 82; Indels 37; Gaps 4;

1 MSSCRVNGVMPRLNLSASRRNHEMDESAQPLPPASVGGGGGASPSAAAAAAS 60
 175 mssckysgymkplrsfssrrnlleaeegqlp-----lsp----- 213
 61 SSAPEIVSKPEHNSNNALXGTG-----GSGTGGGGGGSGSGSSGSKSKKN 114
 214 snpeltvlsredhahqcllnpnahtnqhagltta-----stlfpnktrn 263
 115 ONIGYKLRRALEKRRRLSDYALIFGEGIVYVETELSMGAYDKASLYSLAKLCI 174
 264 gniyglghrralekrrlsdyallfgmgiyvmveteleawgyskxsmfslakcl 323
 175 SLSTIIIGLIIVHAREIOLFVNDGADWRIAMTEREFICLEIIVCAIHPICNTY 234
 324 slstlllglllyahrltvgqfvdndadwriamterefllslsmlylnhclpgey 383
 235 FWTARLASVAPSTTADVDIISIPMFLRLYLARVMLSKLFTDASSRSGALNKI 294
 384 ffwatrlatfypsrdaedvdlisipmflrlyllarvmlhsklftdassrsgalnki 443
 295 NENREYAKTLMTCIGTYLVFESISIMIIAATVACGRYHDQDVTNFGAMWLISI 354
 444 nhnttfvmltclpgrtvlvflslllaawtvyceeryhdqdvtnflgawmlisi 503
 355 TELSTIGVDWPNYCGKGVCLTIGMAGCTALVAVYARKELETKAEKHVNFMDTQ 414
 504 flstlsgvdwvnycgkgyclltgimgagctalvaavarkelctkækhvndfmmdtq 563
 415 LTRKVNAAANVLEPWLIIKNTKRLKIDAKVKKHOKRFLQAIHOASRKMKORLND 474
 564 ltrklnaaanvlewllykntkrlkldakvkrkhrflqalhoasrkmgqrtsld 623
 475 QANTIVDLAKTONIMWISDLNERSDEPKRIVLEKLETLIGSIHMLPGLISOTIRO 534
 624 qantlvdlaktonimwisdlnersdepkriylekletlignsihmlpglisotiro 683
 535 QORDFEAMESYDKHVTYNERSKSSRRKSSSTAPPTSSESS 579
 684 qgqqlsailearqvaagvtchpisdrlpivssstappts 728

Small conductance calcium-activated potassium channel protein 1;
 hsk1; human; potassium ion flux.

Key Location/Qualifiers
 MISC-difference 164
 /note= "encoded by Arg"

W0981139-A1.
 19-MAR-1998.
 10-SEP-1997; 97MO-US16033.
 17-APR-1997; 97US-0045233.
 11-SEP-1996; 96US-0026451.
 07-MAR-1997; 97US-0040052.

(ICAG-) ICAGEN INC.
 (DOR-) UNIV OREGON HEALTH SCI.
 Adelman JP, Bond CT, Maylie J, Silvia CP;
 WPI: 1998-207332/18.
 N-PSDB: V35445.
 DNA encoding calcium-activated potassium channel - useful in assays
 to identify compounds which increase or decrease potassium ion flux

Claim 2: Page 92-93; 151pp; English.

This sequence is the human small conductance calcium-activated
 potassium channel protein 1 (hsk1) of the invention. The proteins of the
 invention are monomers of a calcium-activated potassium channel, where
 the monomer: (1) has a calculated molecular weight of between 40 and
 80 kDa; and (11) has a unit conductance of between 2 and 60 pS when the
 monomer is in the functional polymeric form of a potassium chain and is
 expressed in a Xenopus oocyte. Antibodies specific for the protein, and
 probes specific for the DNA can be used to detect the presence of the
 protein or DNA sequences in a sample. Host cells expression of the
 protein can be used in assays to identify compounds which increase or
 decrease the potassium ion flux through the protein. The transfected host
 cell can also be used for the recombinant production of the protein. The
 DNA sequences can also be used for determining mutations in the SK and IK
 genes in a computer system. The proteins encoded by the SK and IK genes
 can be used in a computer system for determining their three dimensional
 structure, which is useful for determining ligands that bind to the
 proteins.

Sequence 561 AA:

Query Match 63.3%; Score 1868.5; DB 19; Length 561;
 Best Local Similarity 70.3%; Pred. No. 1.6e-168;
 Matches 378; Conservative 46; Mismatches 79; Indels 35; Gaps 7;
 1 MSSCRVNGVMPRLNLSASRRNHEMDESAQPLPPASVGGGGGASPSAAAAAAS 58
 19 mshsnygsvgplsgpgrald--pppeaghpqppspg-----lqvvaaksepar 71
 59 VSSAPETIVSKPEHNSNNALXGTGSGTGGGGGGSGSGSSGSKSKKNONIG 118
 72 pspgspr--gqpqgdqde-----ddeeagqqragsprrvng 108
 119 YKLGRRALEKRRRLSDYALIFGEGIVYVETELSMGAYDKASLYSLAKLCIIST 178
 109 hrighrralekrrlsdyallfgmgiyvmveteleawgyskxsmfslakclisist 168
 179 IITGLIIVHAREIOLFVNDGADWRIAMTEREFICLEIIVCAIHPICNTYTWT 238
 169 alligtlvlyhareiolfvndgadwriamterefllslslavcaihpypqhyflwt 228

QY 239 ARAFSTADSTTTADVDTIISIPMFLRLYLIRVWLHLSKLETDASSRSIGALNKINFT 298
 Db 229 arlafstadvdtiisipmflrllylrvwlhlskltfdassrsigalklnt 288
 QY 299 RFWMTLMTICPGTVLLVPSISLMTIAAMTVRACERYHDOODVTSNPGAMWLSTSTFS 288
 Db 289 rfwmktlmticpgtvllvpsiswlaawlvrceryhdkqevtsnpgamwlststfs 348
 QY 359 IGYDMVNTYCGCGVCLLTGIMAGCTALVAVVARKLELTKAEKHNHMDTOLTKR 418
 Db 349 igydmvntycgcvclltgimgagctalvavvarkleltkaekehnmfmdtqltkr 408
 QY 419 VKNAANAVLRETWLIYKNKIDAKYRKORKEFLQAIHQ---LRSVKMDORKLNDQ 475
 Db 409 vknaaanvltretwliykntkdkayrkorkrflqaihqsklrsvklegklnq 468
 QY 476 ANTLVDLAKTONIMYDMSIDNERSDEFEKRIYVLETKLETIGSIHALGSLISOTR 533
 Db 469 antldlaktqvmvdyvelshqhelearlatlesrlalgsalqalpqlaqalr 526

RESULT 10

ID W63704 standard; Protein: 458 AA.
 AC W63704;

DT 01-OCT-1998 (first entry)

DE Rat rsk1 protein.

KW Small conductance calcium-activated potassium channel protein 1;

KM rsk1; rat; potassium ion flux.

OS Rattus sp.

PN W0981139-A1.

PD 19-MAR-1998.

PF 10-SEP-1997; 97MO-US16033.

PR 17-APR-1997; 97US-0045233.

PR 11-SEP-1996; 96US-0026451.

PR 07-MAR-1997; 97US-0040052.

PA (ICAG-) ICAGEN INC.

PI (UYOR-) UNIV OREGON HEALTH SCI.

DR Adelman JP, Bond CT, Maylie J, Silvia CP;

DR WPI: 1998-207332/18.

DR N-PSDB; V35448.

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CC can be used in a computer system for determining their three dimensional
 CC structure, which is useful for determining ligands that bind to the
 CC proteins.
 XX
 XX
 SO Sequence 458 AA;

Query Match 59.3%; Score 1752.5; DB 19; Length 458;
 Best Local Similarity 79.0%; Pred. No 1.2e-157;
 Matches 334; Conservative 43; Mismatches 43; Indels 3; Gaps 1;

QY 113 KNQIGYKLGHRALFEKRRKLSQYALIGMGIVVYETELSMGAYDKASTYALKC 172
 Db 3 kptvshrlghrralfekrrklsqyaligmgivvvetelsgaydkastyalkc 62
 QY 173 LISLSTIILGLIIVYHAREIQLEPMYDNGADMRIAMTVERIFCILEILVCAIHPGN 232
 Db 63 lislstvilglivynareqlfivdngadmr iamtervslstelavcalhpngh 122
 QY 233 YTEWTARLASVAPSTTTADVDTIISIPMFLRLYLIRVWLHLSKLETDASSRSIGALN 292
 Db 123 yftwtarlasvpsaaadvdtiisipmflrllylrvwlhlskltfdassrsigaln 182
 QY 293 KINENFRVMTKMTICPGTVLLVPSISLMTIAAMTVRACERYHDOODVTSNPGAMLI 352
 Db 183 kinenfrvmtkmticpgtvllvpsiswlaawlvrceryhdkqevtsnpgamli 242
 QY 353 STEFLSIGYDMVNTYCGCGVCLLTGIMAGCTALVAVVARKLELTKAEKHNHMD 412
 Db 243 stflsigydmvntycgcvclltgimgagctalvavvarkleltkaekehnmfmd 302
 QY 413 TOLTRVKNAAANVLTRETWLIYKNKIDAKYRKORKEFLQAIHQ---LRSVKMD 469
 Db 303 toltrvknnaaanvltretwliykntkdkayrkorkrflqaihqsklrsvklegklnq 362
 QY 470 RKLNQANTLVDLAKTONIMYDMSIDNERSDEFEKRIYVLETKLETIGSIHALGSLIS 529
 Db 363 rklndqantldlakqslayevselqgqelearlatlesrlalgsalqalpqla 422
 QY 530 QRT 532
 Db 423 gal 425

RESULT 11

ID W67823 standard; Protein: 217 AA.
 AC W67823;

DT 25-MAR-1999 (first entry)

DE Human secreted protein encoded by gene 17 clone HFLBA06.

KW Human; secreted protein; fusion protein; gene therapy; protein therapy;

KW diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia;

KW developmental abnormality; foetal deficiency; blood allergy; renal;

KW inflammation; ischaemic shock; Alzheimer's disease; lymphoma;

KW cognitive disorder; schizophrenia; prostate; osteoarthritis; AIDS;

KW osteoporosis; arthritis; testis; lung; thyroiditis; thyroid; digestion;

KW endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.

OS Homo sapiens.

XX

XX

XX

XX

XX

XX

XX

XX

XX

Key Location/Qualifiers
 MISC-difference 217
 /Label= unknown

W09842738-A1.

01-OCT-1998.

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us-09-254-590-19.rag

19-MAR-1998; 98MO-0505311.

XX 30-MAY-1997; 97US-0050937.
 PR 21-MAR-1997; 97US-0041276.
 PR 21-MAR-1997; 97US-0041276.
 PR 21-MAR-1997; 97US-0041281.
 PR 21-MAR-1997; 97US-0042344.
 PR 30-MAY-1997; 97US-0048094.
 PR 30-MAY-1997; 97US-0048095.
 PR 30-MAY-1997; 97US-0048096.
 PR 30-MAY-1997; 97US-0048099.
 PR 30-MAY-1997; 97US-0048131.
 PR 30-MAY-1997; 97US-0048135.
 PR 30-MAY-1997; 97US-0048154.
 PR 30-MAY-1997; 97US-0048160.
 PR 30-MAY-1997; 97US-0048186.
 PR 30-MAY-1997; 97US-0048188.
 PR 30-MAY-1997; 97US-0048350.
 PR 30-MAY-1997; 97US-0048351.
 PR 30-MAY-1997; 97US-0048352.
 PR 30-MAY-1997; 97US-0048355.
 PR 05-AUG-1997; 97US-0054804.
 XX (HUMA-) HUMAN GENOME SCI INC.
 PA Brewer LA, Duan R, Ebner R, Ferrie AM, Florence KA,
 PI Greene JM, Hu JS, Lafleur DM, Moore PA, Ni J, Olsen HS;
 PI Rosen CA, Ruben SM, Shi Y, Young P;
 XX WPI: 1999-070066/06.
 N-PSDB: X00627.
 XX New isolated human genes and the secreted polypeptides they encode -
 PT useful for diagnosis and treatment of e.g. cancers, neurological
 PT disorders, immune diseases, inflammation or blood disorders
 XX
 PS Claim 11: Page 283; 385pp; English.

XX This sequence represents a secreted human protein encoded by the gene
 CC clone detailed in the descriptor line. The gene can be used to generate
 CC fusion proteins by linking to the gene to a human immunoglobulin Fc
 CC portion (e.g. X00602) for increasing the stability of the fused protein
 CC as compared to the human protein only.
 CC The invention relates to 87 novel genes and their fragments (nucleic acid
 CC sequences: X00611-X00724; amino acid sequences W67807-W68004) which
 CC are useful for preventing, treating or ameliorating medical conditions
 CC e.g. by protein or gene therapy. Also, pathological conditions in a sample
 CC diagnosed by determining the amount of the new polypeptides in a sample
 CC or by determining the presence of mutations in the new polynucleotides.
 CC Specific uses are described for each of the 87 polynucleotides, based on
 CC which tissues they are most highly expressed in (see X00611 for described
 CC uses).

XX Sequence 217 AA;
 SQ

Query Match 32.7%; Score 964.5; DB 20; Length 217;
 Best Local Similarity 90.0%; Pred. No. 2,3e-83; Indels 15; Gaps 1;
 Matches 189; Conservative 4; Mismatches 2;

QY 262 MFLRLYLIALRVMLLSKLTFTDASSRISGALNKINFTREVMKTLMTICPGTVLAFRSISL 321
 DB 1 MFLRLYLIALRVMLLSKLTFTDASSRISGALNKINFTREVMKTLMTICPGTVLAFRSISL 60
 QY 322 WIIAAWTVRACER-----YHODDVSNFLGAMMLDITSTLSIGYGDMP 366
 DB 61 WIIAAWTVRACER-----YHODDVSNFLGAMMLDITSTLSIGYGDMP 120
 QY 367 NTYCGKVCGLLGGINGAGCTALVAVAKLELTKAKAHNFMMDPTOLTRVYNAANV 426
 DB 121 htycgkvccllgtngagcctalvavarkleltkaaeknhnmmdptqltrklnaanv 180

QY 427 LRETWLIYKNTKLVKKIDHAKVRHQRKFL 456
 DB 181 lretwliykntklvkkidhavrhrkqkfl 210

RESULT 12
 ID W98019 standard; Protein: 425 AA.
 W98019;
 AC W98019;
 XX 21-JUN-1999 (first entry)
 DE Mouse calcium activated potassium channel Kca4 orthologue.
 XX Calcium activated potassium channel; Kca4; mouse; leukocyte.
 OS Mus sp.
 XX W09903882-A2.
 PN W09903882-A2.
 XX 28-JAN-1999.
 PD 28-JAN-1999.
 XX 13-JUL-1998; 98MO-GB02058.
 PF 13-JUL-1998; 98MO-GB02058.
 PR 09-OCT-1997; 97GB-0021366.
 PR 15-JUL-1997; 97GB-0014760.
 XX (ZENEC) ZENEC LTD.
 PA Aiyar J, Logsdon NJ;
 PI WPI: 1999-132158/11.
 N-PSDB: X24831.
 DR New isolated leukocyte calcium activated potassium channel nucleic
 XX acids - used to develop products for treating e.g. inflammation,
 PT asthma, allergies, graft rejection, proliferative disorders,
 PT neurodegenerative diseases or autoimmune diseases
 XX
 PS Example 18: Page 102-103; 139pp; English.

XX The present sequence is the murine orthologue of a novel human
 CC calcium activated potassium channel (CACC) designated hKca4 (see
 CC W98017). The sequence was deduced from a full-length cDNA clone
 CC (see X24831) amplified from mouse erythroleukemic cell line
 CC MEL-C88 cDNA. The invention also provides expression vectors and
 CC antisense molecules, host cells, purified polypeptides and
 CC polynucleotides, antibodies and (ant)agonists of CACC function.
 CC Compounds that modulate CACC activity can be used in treating
 CC diseases which are manifested by dysfunctional leukocytes.

XX Sequence 425 AA;
 SQ

Query Match 30.2%; Score 893.5; DB 20; Length 425;
 Best Local Similarity 44.3%; Pred. No. 3,7e-76; Indels 33; Gaps 6;
 Matches 189; Conservative 69; Mismatches 136;

QY 121 LGHRRALFEKRRKSLDYALIFGMGIVWVITELSMGAVDKASLSLAKTISTSTII 180
 DB 12 lrrkrlleqekrswgawlaigtglmvlhaemlflgckwlylllvkcllslstaf 71
 QY 181 ILGLIIVYHAREIOLFMVNDGADWRKAMRYERIFLELIVCAHHP-----G 231
 DB 72 ILGLIIVYHAREIOLFMVNDGADWRKAMRYERIFLELIVCAHHP-----G 231
 QY 232 NTYTF--WTARLAFSAFSTTADVDIILSPFRLYLIALRVMLLSKLTFTDASSRISG 289
 DB 132 eadqapppgfl-----gegaallslamlrllylvpravlrsylnaasyrsig 181
 QY 290 ALNKINFTREVMKTLMTICPGTVLAFRSISLWIIAAWTVRACERHODDVSNFLGAM 349

Query Match	29.8%	Score 880.5	DB 20	Length 427	
Best Local Similarity	43.4%	Pred. No. 6.3e-75		Gaps 43	7
Matches 188	Conservative	71	Mismatches 131	Indels	
121	LGRRALFEKRRLSDVALFGMFGIYVWVLEETLSGADVANDASYSIALKCLISLSTII	180			
07	LGRRALFEKRRLSDVALFGMFGIYVWVLEETLSGADVANDASYSIALKCLISLSTII	180			

```

Db      12 lrrkrllbeqeslagwvalaagvtgltmvlhaemlwfqgcswalylflvkcslstsfll 71
Oy      181 lrlgllyvHAREtOLrPDNADNMRlMARErRfFtCtEllyVCAHrP----- 230
Db      72 llcllvahakevgqlfmlclnglrlowrvaltqgaqvalvclavcgllhapvrgpccvdl 131
Oy      231 GNTFTWArLArLArSVArSTT-----TADVlllSPMLrRyLArLArMlLHskLFtDA 283
Db      132 g-----aplspwpgvflgagellslsmlllrrlyprxavllrsgvllna 177
Oy      284 SRSICALINKrNFrMKTlMTlCGrVlLrFVSllMlTArLArRACErRHODvRtS 343
Db      178 syrslyabgrvrlhwfvaklymrbhgrlllglvlgwlltawlvsvae--qavnatg 235
Oy      344 nrlGAWMLlStFtLStSlGDMrPNrTCCGKvCLlTGlMAGCtAlvVAVArKLElKAE 403
Db      236 hslclwllprlfltllygvgdvprgltmavklyclctgmsvcccllvaavakrlfelnhae 295
Oy      404 KHVrNEMPDOLrCtRvKNAANArLrETWllyKNTKlLArKIDArVrKHOKRtOLArHOLr 463
Db      296 kvrvmrmmddlyrlkemksaearylgeawmflfkyhr--rshsa-arbhqklllaatnafr 352
Oy      464 svKvKDLrMDANrLrDLArLArTONlMvArDlSDlRNSERSEDEKRIvTLEKLEllLGSIsA 523
Db      353 gvrllhkrklrlegvsmvdrksmmllyddqnlslsmralekql-----dlaagklida 405
Oy      524 lPGLlSOTrRQOQ 536
Db      406 lteellstalprrq 418

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CC	Potassium channel, where the monomer: (1) has a calculated molecular
XX	
PS	Claim 2; Page 117-118; 15ipp; English.
XX	
CC	This sequence represents the human intermediate conductance
CC	calcium-activated potassium channel protein 1 (hik1) of the invention
CC	The proteins of the invention are monomers of a calcium-activated
XX	
PR	DNA encoding calcium-activated potassium channel - useful in assays
PT	to identify compounds which increase or decrease potassium ion flux
PT	
DR	N-PSDB; V35463.
XX	
XX	WPI; 1998-207332/18.
XX	
PI	Adelman JP, Bond CT, Maylie J, Silvia CP;
XX	
PA	(UCOR-) UNIV OREGON HEALTH SCI.
XX	
XX	(ICAG-) ICAGEN INC.
XX	
PF	10-SEP-1997; 97WO-US16033.
XX	
XX	17-APR-1997; 97US-0045233.
PR	11-SEP-1996; 96US-0026451.
PR	07-MAR-1997; 97US-0040052.
XX	
PN	WO981139-A1.
XX	
PD	19-MAR-1998.
XX	
OS	Homo sapiens.
XX	
KX	Intermediate conductance calcium-activated potassium channel protein 1;
XX	hik1; human; potassium ion flux.
DE	
XX	Human hik1 protein.
DF	
XX	01-OCT-1998 (first entry)
AC	
XX	W63713;
ID	W63713 standard; Protein; 428 AA.
RESULT	15

Sequence 428 AA;

Matches 186; Conservatively 73; Pred. No. 7e-73; Length 428;

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Db      406 altelstajprq 419

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Job time: 4472 sec

Page 1

QY 468 GTGGGCGCCACGAACAAGCCTGCCTTGTTCATTTT

||||| ||| |||| | |||| |||| |||| |||| |||| ||||

Db 1201 ttggggttctactcaagaagccatcgttcttggccctgaatgacgtatcagct 1260
Qy 528 CTCACGATCATCTGCTGGTGTGATCATCGTACGACCCGAGGAATACACTGTT 587
Db 1261 gtccacataatccttcttgctgtatcatcgccacacacacgagtgacagctct 1320
Qy 588 CATGTGACAAATGAGCAGACGACTGAGGAATAGCCATGACTTATGACCTGTTCTT 647
Db 1321 cgtatcgaacaagcagcgagatgactcgtcgatgacatgacacagagccatccta 1380
Qy 648 CATCTGCTTGAATACTGCTGTGCTTATTCATTCATCCATACCTGGGAATTAATACATC 707
Db 1381 catlagccgagagatgctgtgtacacacacacacacattccgtcgagatcaagctct 1440
Qy 708 ATGAGAGCCCGGCTTCTCTCTATGATCCCATCCACACACCCGCTGATGATGAT 767
Db 1441 ctgggagcagccttgctctctacacacccctcccgagcgagagccagctgagcat 1500
Qy 768 TATTTATCTATACCAATGTTCTTAAGACTCTATGATGATGATGATGATGATGAT 827
Db 1501 catctgtctatcccatcgttctcgtcgtcgtacgtacgtacgtacgtacgtacgtac 1560
Qy 828 TAGCAACTTTTACCTGATGCTCTCTCTAGAACATTTGAGACATTAATAGATAACTT 887
Db 1561 cagcagactctcagatgctcgtcccgagcagcagcagcagcagcagcagcagcagc 1620
Qy 888 CAATACAGCTTTTGTATGAGACTTAAATGATGATGATGATGATGATGATGATGAT 947
Db 1621 caaacacccgtctgtacatgagcagcagcagcagcagcagcagcagcagcagcagc 1680
Qy 948 TTTTATCTATACCAATGTTCTTAAGACTCTATGATGATGATGATGATGATGATGAT 1007
Db 1681 gttcagatctctcgtgtacatcgtcgtcgtacgtacgtacgtacgtacgtacgtac 1740
Qy 1008 TGATCAACAGATGTTTACTAGCAACTCTCTGAGCAGATGATGATGATGATGATGAT 1067
Db 1741 tggcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 1800
Qy 1068 TCTCTCATTTGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1127
Db 1801 ccttccatctgttctgtgagcagcagcagcagcagcagcagcagcagcagcagcagc 1860
Qy 1128 ACTTACTGATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1187
Db 1861 cctcactgtcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 1920
Qy 1188 GCTAGACCTTACCAAGCAGAAACAGTGCACATTTGATGATGATGATGATGATGATGAT 1247
Db 1921 gctgagactccacaaagcagcagcagcagcagcagcagcagcagcagcagcagc 1980
Qy 1248 TAAAGAGTAAATAATGACAGTGCATGATGATGATGATGATGATGATGATGATGAT 1307
Db 1981 caagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 2040
Qy 1308 TACAAAGCTACTGAAATAATGATGATGATGATGATGATGATGATGATGATGATGAT 1367
Db 2041 cctcaagactcgtacaaagatgacatgacatgacatgacatgacatgacatgacat 2100
Qy 1368 GCAAGCTATTCATTAATGAGAGTAAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1427
Db 2101 ccaagcatalccacagcttgagagcgctcaagatgacatgacatgacatgacatgac 2160
Qy 1428 AAACACTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2187
Db 2161 caaacctcgtgagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcag 2220
Qy 1488 AAAG 1547
Db 2221 caatgagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 2280
Qy 1548 TTTTATCTATACCAATGTTCTTAAGACTCTATGATGATGATGATGATGATGATGAT 1607
Db 2281 tctacacgagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 2340

Qy 1608 GAGAGATTTGATGAGGCTGATGAGAG 1635
Db 2341 gcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 2368

RESULT 2
US-09-115-446-5
Sequence 5, Application US/09115446
Patent No. 6165719
GENERAL INFORMATION:
APPLICANT: Chandy, George K.
APPLICANT: Gargus, Jay J.
APPLICANT: Gutman, George
APPLICANT: Pantino, Emmanuelle
APPLICANT: Kalman, Kalatin
TITLE OF INVENTION: HKCA3/KCN3 SMALL CONDUCTANCE CALCIUM
TITLE OF INVENTION: ACTIVATED POTASSIUM CHANNEL: A DIAGNOSTIC
FILE REFERENCE: 07306/014001
CURRENT APPLICATION NUMBER: US/09/115,446
EARLIER FILING DATE: 1998-07-14
EARLIER APPLICATION NUMBER: 60/052,556
EARLIER FILING DATE: 1997-07-15
EARLIER APPLICATION NUMBER: 60/070,741
NUMBER OF SEQ ID NOS: 15
SOFTWARE: PASTSEQ for Windows Version 4.0
SEQ ID NO 5
LENGTH: 2526
TYPE: DNA
ORGANISM: Homo sapiens
US-09-115-446-5

Query Match 44.0%; Score 765.6; DB 4; Length 2526;
Best Local Similarity 73.0%; Pred. No. 3,9e-183;
Matches 984; Conservative 0; Mismatches 364; Indels 0; Gaps 0;

Qy 288 TGGCGGAGCGGCGGACGACGACGACGACGACGACGACGACGACGACGACGACGACGAC 347
Db 1026 tggcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 1085
Qy 348 CATGGCTACAGCTGAGCGGACCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 407
Db 1086 catggtcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 1145
Qy 408 CTACGCGCTCATCTGCGCATGTTGCGCATGTTGCGCATGTTGCGCATGTTGCGCATGTTG 467
Db 1146 ctatgctcgtatcttggagatgattgagatgattgagatgattgagatgattgagatg 1205
Qy 468 GTGGGCGGCGGCGGACGACGCGGCTGCTGATGATGATGATGATGATGATGATGATGAT 527
Db 1206 ttgggttctgtacaaagactcagctcagctcagctcagctcagctcagctcagctc 1265
Qy 528 CTCACGATCATCTGCTGGTGTGATCATCGTACGACCCGAGGAATACACTGTT 587
Db 1266 gtccacataatccttcttgctgtatcatcgccacacacacgagtgacagctct 1325
Qy 588 CATGTGACAAATGAGCAGACGACTGAGGAATAGCCATGACTTATGACCTGTTCTT 647
Db 1326 cgtatcgaacaagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcag 1385
Qy 648 CATCTGCTTGAATACTGCTGTGCTTATTCATTCATCCATACCTGGGAATTAATACATC 707
Db 1386 catlagccgagagatgctgtgtacacacacacacacattccgtcgagatcaagctct 1445
Qy 708 ATGAGAGCCCGGCTTCTCTCTATGATCCCATCCACACACCCGCTGATGATGATGAT 767
Db 1446 ctgggagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 1505
Qy 768 TATTTATCTATACCAATGTTCTTAAGACTCTATGATGATGATGATGATGATGATGAT 827


```

; GENERAL INFORMATION:
; APPLICANT: ERTESVAG, HELGA
; APPLICANT: VALLA, SVEIN
; APPLICANT: SKJAK-BRAEK, GUDMUND
; APPLICANT: LARSEN, BJORN
; TITLE OF INVENTION: DNA COMPOUNDS COMPRISING SEQUENCES
; TITLE OF INVENTION: ENCODING MANNUROMAN C-5-EPIMERASE
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BIRCH, STEWART, KOLASCH & BIRCH, LLP
; STREET: P.O. BOX 747
; CITY: FALLS CHURCH
; STATE: VA
; COUNTRY: USA
; ZIP: 22042
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentln Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/387,942C
; FILING DATE: 09-MAY-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: MURPHY JR, GERALD M.
; REGISTRATION NUMBER: 28,977
; REFERENCE/DOCKET NUMBER: 1809-106P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-205-8000
; TELEFAX: 703-205-8050
; INFORMATION FOR SEQ ID NO: 35:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 459 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-387-942C-35

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Query Match          3.5%; Score 61.2; DB 2; Length 459;
Best Local Similarity 51.2%; Pred. No. 2.1e-06;
Matches 169; Conservative 0; Mismatches 158; Indels 3; Gaps 1;
QY 157 GCTGCGCGCGCGCGCTGTTCTGCTCAAGCCCGGAGATCTGTGTCTAAGCCCGAG 216
DB 13 GCGGGGACAAAGCCCTGCTCGTCTGCGCGCGGAGACATCTGTCGCGCCACCGCGGC 72
QY 217 CACACAACTCTCAACAACTGCTCTATGGAACCGCGCGGAGAGAGACTGGAGGA 276
DB 73 AAGCAGACGCTCGACGCGCGCGCGGACGACATCTGTCGCGCGCGCGCGCGCGC 132
QY 277 GCGCGCGCGGTGCGGAGCGGAGCGGAGCGAGAGAGTGGACCAAGTCCAGCAAAAAG 336
DB 133 ACCCTCAACGGCGCGCGCGGAGCGGAGCTGTTCCGCTTCGAGCGCTGTCGACACG 192
QY 337 AAAAACCAGAACTCGGCTCAAGCTGGGCGACCGCGCGCGCTGTTGAAAAAGCGC-- 393
DB 139 GCGCACTAGACATCGCGGACAAACAGGCGGACCGCATCGCGACTTCGCGGTGGCGCA 252
QY 394 AAGCGGCTCAGCGACTACGCGCTCATCTTGGCATGTTGGCATCCGTGTCATGTGTCATC 453
DB 253 GACAAAGCTCGAGGTATCGCGGCTTACCGGCTGGGCGAGCGGCTACAAAGGCGCAC 312
QY 454 GAGACCGAGCTGTCGTGGGCGCGCTTACGAC 483
DB 313 CTCGCGCTGTGCTCAACAGCGCGCGGCGAC 342

```

RESULT 5
US-08-387-942C-1
Sequence 1, Application US/08387942C

```

; Patent No. 5939289
; GENERAL INFORMATION:
; APPLICANT: ERTESVAG, HELGA
; APPLICANT: VALLA, SVEIN
; APPLICANT: SKJAK-BRAEK, GUDMUND
; APPLICANT: LARSEN, BJORN
; TITLE OF INVENTION: DNA COMPOUNDS COMPRISING SEQUENCES
; TITLE OF INVENTION: ENCODING MANNUROMAN C-5-EPIMERASE
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BIRCH, STEWART, KOLASCH & BIRCH, LLP
; STREET: P.O. BOX 747
; CITY: FALLS CHURCH
; STATE: VA
; COUNTRY: USA
; ZIP: 22042
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentln Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/387,942C
; FILING DATE: 09-MAY-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: MURPHY JR, GERALD M.
; REGISTRATION NUMBER: 28,977
; REFERENCE/DOCKET NUMBER: 1809-106P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-205-8000
; TELEFAX: 703-205-8050
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12588 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; ORIGINAL SOURCE:
; ORGANISM: Azotobacter vinelandii
; STRAIN: E
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 290..1951
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 2227..6438
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 6702..9695
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 9973..12588
US-08-387-942C-1

```

```

Query Match          3.5%; Score 61.2; DB 2; Length 12588;
Best Local Similarity 51.2%; Pred. No. 1e-05;
Matches 169; Conservative 0; Mismatches 158; Indels 3; Gaps 1;
QY 157 GCTGCGCGCGCGCGCTGTTCTGCTCAAGCCCGGAGATCTGTGTCTAAGCCCGAG 216
DB 8322 GCGGGGACAAAGCCCTGCTCGTCTGCGCGCGGAGACATCTGTCGCGCCACCGCGGC 8381
QY 217 CACACAACTCTCAACAACTGCTCTATGGAACCGCGCGGAGAGAGACTGGAGGA 276
DB 8382 AAGCAGACGCTCGACGCGCGGCGCGGACGACATCTGTCGCGCGCGCGCGCGGCG 8441
QY 277 GCGCGCGCGGTGCGGAGCGGAGCGGAGCGGAGAGTGGACCAAGTCCAGCAAAAAG 336
DB 8442 AGCCTCAGCGGCGCGCGGAGCGGAGCGGAGCGTGTTCGCTTCGAGCGCGCTGTCGACAGCGCAG 8501

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Db 916 GCCGCCGCCGATGCCGTGCCACCTGCCCCGCCGAGGCCGCCGCCGTGGCTGCCGCG 857

Qy 178 TCGTCCTCAGCCCCCGAGATCGTGTCTTAAGCCCGACACAACTCTCAAAACCTG 237

Db 856 CGGTGATCGCGCCGCGCCACACAGCCCGGGTGTGGGAGCCCGAGCGCATGTTCAATG 797

Qy 238 GCGCTCTTATGGAACCGCGCGGCGAGGAGCAGCACTGAGAGGCGCGCGCTGGCGGAGAC 297

Db 796 GCGGCGCGCGCGCGGGGGTGGACAGATGGGCCAGGCTGTGATATATCGGGGTGAGGGTGC 737

Qy 298 GGGCAGCGGACAGCAGC 314

Db 737 GCGGCGCGCTTACAG 720

PACIFIC

US-09-206-537-7/c
; Sequence 7, Application US/09206537

GENERAL INFORMATION:

APPLICANTI: VAN DATUM: 1999

APPLICANT: De Smet, Charles

ADRIENNE BOON Thierry

TITLE OF INVENTION: ELECTRIC MOTOR

CORRESPONDENCE ADDRESS:

600 Atlantic Avenue

CLIFF: BOSCO.

COUNTRY: US

CONFIDENTIAL

MEDIUM TYPE: floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

GRUPEMENT APPLICATION DATA:

APPLICATION NUMBER: 00/00/000000

CLASSIFICATION:

ADD TO CATION NUMBER. 08/845.996

FILLING DATE: 11/11/2007

NAME: Van Amsterdam, John R.

REFERENCE / DOCKET NUMBER: T.0461/7008

TELECOMMUNICATION INFORMATION;

TELEFAX: (617) 720-2441

THE ORIGINAL SOURCE OF ALL INFORMATION

LENGTH: 4524 base pairs

STRANDEDNESS: double

[illegible]

HYPOTHETICAL: NO

FEATURE:

NAME/REL.	DOB	1433
174		

US-09-206-537-7

Quely Marci

Matches	129;	Conservative	0;	Misclassified

58 TTTTCTGGAACCTGTGCACGAGATGGACTCAGH

100

Db 976 TCGCGGGGTCGTCCTCCAGTCCAGATGAGACCCGCGCCGTCGCCCCACCCAGCGGC 917
Qy 118 GTGGAGGAGTGGCGCGCGCGCTCTCCCTCTTCAGACCGCTGCCCGCGCGCGCTTT 177
Db 916 GCGCGCGCGCGCTCTCCAGTCCAGATGAGACCCGCGCCGTCGCCCGCGCGCTTT 177
Qy 178 TCGTCTCAGCGCGCGCGCTCTTCAGTCCAGATGAGACCCGCGCGCGCTTT 237
Db 856 CGGTGTCGCGCGCGCGCTCTTCAGTCCAGATGAGACCCGCGCGCGCTTT 797
Qy 238 GCGCTCTATGGAACCGCGCGCGCGCTCTTCAGTCCAGATGAGACCCGCGCGCGCTTT 797
Db 796 GCGCGCGCGCGCGCGCGCTCTTCAGTCCAGATGAGACCCGCGCGCGCTTT 797
Qy 298 GCGCGCGCGCGCGCGCGCTCTTCAGTCCAGATGAGACCCGCGCGCGCTTT 737
Db 736 GCGCGCGCGCGCGCGCGCTCTTCAGTCCAGATGAGACCCGCGCGCGCTTT 737

RESULT 8

US-08-387-942C-31
; Sequence 31, Application US/08387942C
; Patent No. 5939289

GENERAL INFORMATION:
APPLICANT: ERTESVAG, HELGA
APPLICANT: VALLA, SVEIN
APPLICANT: SKJAK-BRAEK, GUDMUND
TITLE OF INVENTION: DNA COMPOUNDS COMPRISING SEQUENCES
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSEE: BIRCH, STEWART, KOLASCH & BIRCH, LLP
STREET: P.O. BOX 747
CITY: FALLS CHURCH
STATE: VA
COUNTRY: USA
ZIP: 22042
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/387,942C
FILING DATE: 09-MAY-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MURPHY JR, GERALD M.
REGISTRATION NUMBER: 28,977
REFERENCE/DOCKET NUMBER: 1809-106P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-205-8000
TELEFAX: 703-205-8050
INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
LENGTH: 459 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-387-942C-31

Query Match 2.7%; Score 47.4; DB 2; Length 459;
Best Local Similarity 49.5%; Pred. No. 0.0063;
Matches 151; Conservative 0; Mismatches 151; Indels 3; Gaps 1;

Qy 182 CTTACGCGCGCGCGCGCGCTCTTCAGTCCAGATGAGACCCGCGCGCGCTTT 241
Db 38 CCGAGCGCGCGCGCGCGCGCTCTTCAGTCCAGATGAGACCCGCGCGCGCTTT 97

Qy 242 TCTATGACACCGCGCGCGCGCTCTTCAGTCCAGATGAGACCCGCGCGCGCTTT 301
Db 98 GCGAGACATCTCTGTCGCGCGCGCGCGCGCTCTTCAGTCCAGATGAGACCCGCGCGCGCTTT 157
Qy 302 ACGGAGGAGTGGCGCGCGCGCTCTTCAGTCCAGATGAGACCCGCGCGCGCTTT 361
Db 158 ACGTGTCTCGCTTTCAGTCCAGATGAGACCCGCGCGCGCTTT 217
Qy 362 TGGGAGGAGTGGCGCGCGCGCTCTTCAGTCCAGATGAGACCCGCGCGCGCTTT 418
Db 218 ACGGAGGAGTGGCGCGCGCGCTCTTCAGTCCAGATGAGACCCGCGCGCGCTTT 277
Qy 419 TCTTTCGCGCGCGCGCGCGCTCTTCAGTCCAGATGAGACCCGCGCGCGCTTT 478
Db 278 GCTTTCGCGCGCGCGCGCGCTCTTCAGTCCAGATGAGACCCGCGCGCGCTTT 337
Qy 479 ACGAG 483
Db 338 GCGAG 342

RESULT 9

US-08-387-942C-9
; Sequence 9, Application US/08387942C
; Patent No. 5939289

GENERAL INFORMATION:
APPLICANT: ERTESVAG, HELGA
APPLICANT: VALLA, SVEIN
APPLICANT: SKJAK-BRAEK, GUDMUND
TITLE OF INVENTION: DNA COMPOUNDS COMPRISING SEQUENCES
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSEE: BIRCH, STEWART, KOLASCH & BIRCH, LLP
STREET: P.O. BOX 747
CITY: FALLS CHURCH
STATE: VA
COUNTRY: USA
ZIP: 22042
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/387,942C
FILING DATE: 09-MAY-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MURPHY JR, GERALD M.
REGISTRATION NUMBER: 28,977
REFERENCE/DOCKET NUMBER: 1809-106P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-205-8000
TELEFAX: 703-205-8050
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 459 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-387-942C-9

Query Match 2.6%; Score 44.6; DB 2; Length 459;
Best Local Similarity 45.8%; Pred. No. 0.032;
Matches 192; Conservative 0; Mismatches 224; Indels 3; Gaps 1;

Qy 182 CTTACGCGCGCGCGCGCGCTCTTCAGTCCAGATGAGACCCGCGCGCGCTTT 241
Db 38 CCGAGCGCGCGCGCGCGCGCTCTTCAGTCCAGATGAGACCCGCGCGCGCTTT 97

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HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Human
TISSUE TYPE: Spleen tissue from healthy human
FEATURE:
NAME/KEY: CDS
LOCATION: 1810..1982
FEATURE:
NAME/KEY: misc_feature
LOCATION: 543
OTHER INFORMATION: C may be present or absent
FEATURE:
NAME/KEY: Intron
LOCATION: 1980..2150
FEATURE:
NAME/KEY: 5'UTR
LOCATION: 1..1809
US-08-318-837-1

Query Match      2.5%; Score 43.8; DB 2; Length 2150;
Best Local Similarity 45.1%; Pred. No. 0.11;
Matches 16; Conservative 0; Mismatches 197; Indels 0; Gaps 0;

21 CGGGGCGCTCATGCGCCGCTCAGACAACTTGAAGCGCGTCGCCGCAGAACCTTGACAGAT 80
    |||||          |||   |||  |||  |||  |||  |||  |||  |||  |||  |||
2136 CGGGGCGACACCGGGCACCGGACTGGGCTTGGAGAGCGGCCCGCGAGCCCTGCCCCCG 2077
    |||||          |||   |||  |||  |||  |||  |||  |||  |||  |||  |||
81 GGACCTCAGAGGCGCAACCCTCTCAGACCCCGCCGCTCTGTGGAGAGAGTGGCGCGCTC 140
    |||   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
2076 CCCGCCCGCGCGCCGCCCGCCGACAGCTCGCGCGCGGACAGCGAGAGAGGAGG 2017
    |||   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
141 CTCGCCCTCTGACAGCGCGTGCGCCCGCGCGCTGTTGCTCTCAGCCCGCGAATGCT 200
    |||   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
2016 GAGGGGCGCGGGCGGGGGGTGCGCGGACACTCCTCCCTTCCAGCTGCACCGGTC 1957
    |||   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
201 GGTGCTTAAGCCCGAGCACAACACTCCACAACACTGGCGCTCTATGGAACCGCGCGCG 260
    |||   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
1956 GTGGAGTAGTAGCGCCCGCCCGCCCGCCGACAGCGCGCGGACAGAGCAGAGCGG 1897
    |||   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
261 AGGCACACACTGTGAGAGGCGCGCGGTGGCGGAGCGGCGACAGGCAACAGCAAGTGAC 320
    |||   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
1896 GAGTCGCGGGCGGGGCGGCGCGCGGGCGGGGTGCGGCAAGGCTGCCCGCGGGCGCC 1837
    |||   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
321 CAGGTCACAGAAAAAGAAAACGAGAATCGGCTACAGAGCTGGGCGCACCGGCGCGCC 379
    |||   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
1836 CCAGGCGCGCGCGCGCGCGCGCGCGCAATGCTGTGGCGCGGCGCTCGCGCGCGCGCC 1778
    |||   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||

RESULT 11
US-07-945-283-1
Sequence 1, Application US/07945283
Patent No. 5352596
GENERAL INFORMATION:
APPLICANT: Cheung, Andrew K.
APPLICANT: Wesley, Ronald D.
TITLE OF INVENTION: Pseudorabies Virus Deletion Mutants
TITLE OF SEQUENCE: Involving The EPO and LTR Genes
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Curtis P. Ribando
STREET: 1815 No. 5352596th University Street
CITY: Peoria
STATE: IL
COUNTRY: USA
ZIP: 61604
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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US-09-254-590-21

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1 APPLICATION NUMBER: US/07/945,283
2
3 FILING DATE: 19920911
4
5 CLASSIFICATION: 424
6
7 ATTORNEY/AGENT INFORMATION:
8   NAME: Ribando, Curtis P
9
10 REGISTRATION NUMBER: 27976
11
12 TELECOMMUNICATION INFORMATION:
13   TELEFAX: 309-665-4128
14
15 INFORMATION FOR SEQ. ID NO. 1:
16   SEQUENCE CHARACTERISTICS:
17     LENGTH: 8438 base pairs
18     TYPE: NUCLEIC ACID
19     STRANDEDNESS: double
20     TOPOLOGY: linear
21
22 MOLECULE TYPE: DNA (genomic)
23
24 HYDROTHERMAL: NO
25
26 ANTI-SENSE: NO
27
28 ORIGINAL SOURCE:
29   ORGANISM: Pseudorabies virus
30
31 FEATURE:
32   NAME/KEY: CDS
33   LOCATION: 622..6495
34
35 FEATURE:
36   NAME/KEY: variation
37   LOCATION: replace(1099, "g")
38
39 FEATURE:
40   NAME/KEY: variation
41   LOCATION: replace(1267, "t")
42
43 FEATURE:
44   NAME/KEY: variation
45   LOCATION: replace(1381, "c")
46
47 FEATURE:
48   NAME/KEY: variation
49   LOCATION: replace(1566, "c")
50
51 NAME/KEY: variation
52 LOCATION: replace(7010, "g")
53
54 IS-07-945-283-1

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Query Match	2.58;	Score 43.8;	DB 1;	Length 8438;
Best Local Similarity	48.28;			
Matches 123; Conservative	0.11;			

	QY	63	CCGAGACCTTGACACGAGATGACTCTCAGAGGCGAGGCCCTCTGAGGCCGCCGCTCTGTGCG	122		0Y	183	CTCAGCCCGCCGAGATCGTGGTGTCTTAACCCCGACACACACATCTCCAACTCTGGCGCT	242		QY	4074	CGCGCGTCCCGCGGGCGCGCGGCCCGCGCGCGCTCTTCTTCTGTGCGCGCTGGGGG	4133		QY	243	CTATGGAAACCGCGCGGCGAGAGCAGCATGTGAGAGCGCGCGCGCTGTGCGGAGACCGGCA	302		Db	4134	CTGGGCTCGCGGCGCGCGGGGCGAGCTGGCGCTGACCGGAGGAGCGCGAGAGCGGACT	4193		QY	303	CGGACGACGACGTGG	317		Db	4194	TGCTGCGGAGCTGG	4208		QY	3954	CCGAGACGGGCCCCGAGATCTCCAGGAGACCGGCGCTTGCGCGGGGGCCCCCGGCTCTCTTCGT	4013		QY	123	AGAGGTGGCGGCGCGGCTCTCTCCGCTCTCAAGCCGTCGCCGCGCGCGCTGTTTGTC	182		Db	4014	CGTGGCGGAGCGCGCTGGCGCTCTCCCGCGGAGGGCCGAGCGAGAGACCCCTCTGCTCTCT	4073		QY	183	CTCAGCCCGCCGAGATCGTGGTGTCTTAACCCCGACACACACATCTCCAACTCTGGCGCT	242		Db	4074	CGCGCGTCCCGCGGGCGCGCGGCCCGCGCGCGCTCTTCTTCTGTGCGCGCTGGGGG	4133		QY	243	CTATGGAAACCGCGCGGCGAGAGCAGCATGTGAGAGCGCGCGCGCTGTGCGGAGACCGGCA	302		Db	4134	CTGGGCTCGCGGCGCGCGGGGCGAGCTGGCGCTGACCGGAGGAGCGCGAGAGCGGACT	4193		QY	303	CGGACGACGACGTGG	317		Db	4194	TGCTGCGGAGCTGG	4208		QY	63	CCGAGACCTTGACACGAGATGACTCTCAGAGGCGAGGCCCTCTGAGGCCGCCGCTCTGTGCG	122		QY	183	CTCAGCCCGCCGAGATCGTGGTGTCTTAACCCCGACACACACATCTCCAACTCTGGCGCT	242		Db	4074	CGCGCGTCCCGCGGGCGCGCGGCCCGCGCGCGCTCTTCTTCTGTGCGCGCTGGGGG	4133		QY	243	CTATGGAAACCGCGCGGCGAGAGCAGCATGTGAGAGCGCGCGCGCTGTGCGGAGACCGGCA	302		Db	4134	CTGGGCTCGCGGCGCGCGGGGCGAGCTGGCGCTGACCGGAGGAGCGCGAGAGCGGACT	4193		QY	303	CGGACGACGACGTGG	317		Db	4194	TGCTGCGGAGCTGG	4208		QY	3954	CCGAGACGGGCCCCGAGATCTCCAGGAGACCGGCGCTTGCGCGGGGGCCCCCGGCTCTCTTCGT	4013	
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RESULT 12
US-08-118-200-1/c
; Sequence 1, Application US/08118200
; Patent No. 6197500
; GENERAL INFORMATION:
; APPLICANT: SUTHERLAND, Grant R
; APPLICANT: RICHARDS, Robert I

```

1  APPLICANT: SCHLESSINGER, David
2  APPLICANT: NAGARAJA, Ramajiah
3  APPLICANT: KREMER, Eric J
4  APPLICANT: YU, Sul
5  APPLICANT: BAKER, Elizabeth
6  APPLICANT: MULLEY, Jean C
7  APPLICANT: MANDEL, Jean-Louis
8  APPLICANT: PRITCHARD, Melanie April
9  APPLICANT: LYNCH, Michael
10 TITLE OF INVENTION: DNA SEQUENCES RELATED TO ISOLATED
11 TITLE OF INVENTION: FRAGILE X SYNDROME
12 NUMBER OF SEQUENCES: 13
13 CORRESPONDENCE ADDRESS:
14 ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
15 STREET: P. O. Box 1404
16 CITY: Alexandria
17 STATE: Virginia
18 COUNTRY: United States
19 ZIP: 22113-1404
20 COMPUTER READABLE FORM:
21 MEDIUM TYPE: Floppy disk
22 COMPUTER: IBM PC compatible
23 OPERATING SYSTEM: PC-DOS/MS-DOS
24 SOFTWARE: PatentIn Release #1.0, Version #1.25
25 CURRENT APPLICATION DATA:
26 APPLICATION NUMBER: US/08/118,200
27 FILING DATE: 09-SEP-1993
28 CLASSIFICATION: 435
29 PRIOR APPLICATION DATA:
30 APPLICATION NUMBER: US 07/802,650
31 FILING DATE: 05-DEC-1991
32 PRIOR APPLICATION DATA:
33 APPLICATION NUMBER: US 07/672,232
34 FILING DATE: 20-MAR-1991
35 PRIOR APPLICATION DATA:
36 APPLICATION NUMBER: US 07/638,518
37 FILING DATE: 04-JAN-1991
38 PRIOR APPLICATION DATA:
39 APPLICATION NUMBER: US 07/966,517
40 FILING DATE: 23-DEC-1992
41 ATTORNEY/AGENT INFORMATION:
42 NAME: Crane-Feury, Sharon E
43 REGISTRATION NUMBER: 36,113
44 REFERENCE/DOCKET NUMBER: 020160-164
45 TELECOMMUNICATION INFORMATION:
46 TELEPHONE: (703) 836-6620
47 TELEFAX: (703) 836-2021
48 INFORMATION FOR SEQ ID NO: 1:
49 SEQUENCE CHARACTERISTICS:
50 LENGTH: 1028 base pairs
51 TYPE: nucleic acid
52 STRANDEDNESS: single
53 TOPOLOGY: linear
54 MOLECULE TYPE: DNA (genomic)
55 US-08-118-200-1

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Query Match	2.5%	Score 43.6;	DB 4;	Length 1028;
Best Local Similarity	52.2%	Pred. No. 0	084.	

	matches	y/y; Conservative	0; Mismatches	89; Indels	0; Gaps	0;
QY	29	TCATGCGGCGCGCTGACGACTTGAAGCGGTCGCCGCGAATCTCAGAGAAATGAGCTAG	88			
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QY	89	AGGCGGAGCCCTGTCAGCCCGCGCGTGTGCGGAGAGAGTGGGCGCGTCTCCCTG	148			
Db	465	CCGCGCCCGCACG	406			
QY	149	CTGACAGCGCTGCGCGCGCGCGCGCGCTGTTTCGTCCTCAGCCCCGAGATCGATGATCTA	208			
Db	405	CCGCTGAGCTG	346			

Tue May 15 08:41:32 2001

us-09-254-590-21.nli

Page 10

LOCATION: 1. 3468
OTHER INFORMATION: /product= "Full-length pure maize
OTHER INFORMATION: optimized synthetic Bt"
OTHER INFORMATION: /note= "Disclosed in Figure 3 as syn17.mze"
US-07-951-715A-2

Query Match 2.5%; Score 43.2; DB 1; Length 3468;
Best Local Similarity 48.8%; Pred. No. 0.19;
Matches 117; Conservative 0; Mismatches 123; Indels 0; Gaps 0;

QY 211 CCCGAGCAGCAACACTCCAAACCTGGCGCTCTATGAAACCGGGGCGGAGCAGCACT 270
DB 793 CGCGAGATCTACACCAACCCCTGTGTGGAGAACTTGACGGGAGTTCCCGGCGAGCCG 852
QY 271 GGAGGAGCGCGCGCGCGGTGGCGGAGCGGCGGAGCAGCAGTGGCAGCAATCCAGC 330
DB 853 CAGGGCATCGAGGGGAGCATCCGACAGCCCGCCAGCTGATGAGACATCTGAACAGCATCAC 912
QY 331 AAAAGAAAAAACCAACATCGCTACAGCTGGGCGCACCGCGCGCGCTGTGAAAG 390
DB 913 ATCTACACCGACCGCCCGCGGAGTACTACTGAGCGGCGCACAGATCATGGCCAGC 972
QY 391 CGCAAGCGCTCAGCGACTACCGCTCTATCTGGCATGTTCGGGATCGGTGATGTC 450
DB 973 CCCGTGGCTTCAGCGCGCCCGAGTTACCTTCCCTGTACGCGACATGGGCAAGCC 1032

RESULT 15

US-08-459-448A-2
Sequence 2, Application US/08459448A
Patent No. 5859336

GENERAL INFORMATION:

APPLICANT: Kozel, Michael G.
APPLICANT: Desai, Nalin M.
APPLICANT: Lewis, Kelly S.
APPLICANT: Kramer, Vance C.
APPLICANT: Warren, Gregory W.
APPLICANT: Eyoia, Stephen V.
APPLICANT: Crossland, Lyle D.
APPLICANT: Wright, Martha S.
APPLICANT: Merill, Ellis J.
APPLICANT: Launls, Karen L.
APPLICANT: Rothstein, Steven J.
APPLICANT: Bowman, Cindy G.
APPLICANT: Dawson, John L.
APPLICANT: Dunder, Erik M.
APPLICANT: Pace, Gary M.
TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED
NUMBER OF SEQUENCES: 94
TITLE OF INVENTION: INSECTICIDAL ACTIVITY IN MAIZE
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 5859336artis Corporation
STREET: Patent & Trademark Dept., 520 White Plains
CITY: Tarrytown
STATE: New York
COUNTRY: USA
ZIP: 10591-9005

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08459448A
FILING DATE: 02-JUN-1995
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/951,715
FILING DATE: 25-SEP-1992
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/772,027
FILING DATE: 04-OCT-1991
ATTORNEY/AGENT INFORMATION:
NAME: Pace, Gary M.
REGISTRATION NUMBER: 40403
REFERENCE/DOCKET NUMBER: CGC 1577/CIP/DIV4
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919)541-8582
TELEFAX: (919)541-8689
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 3468 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "Synthetic DNA"
HYPOTHEICAL: NO
FEATURE:
NAME/KEY: misc-feature
LOCATION: 1. 3468
OTHER INFORMATION: /product= "Full-length pure maize
OTHER INFORMATION: optimized synthetic Bt"
OTHER INFORMATION: /note= "Disclosed in Figure 3 as syn17.mze"
US-08-459-448A-2

Query Match 2.5%; Score 43.2; DB 2; Length 3468;
Best Local Similarity 48.8%; Pred. No. 0.19;
Matches 117; Conservative 0; Mismatches 123; Indels 0; Gaps 0;

QY 211 CCCGAGCAGCAACACTCCAAACCTGGCGCTCTATGAAACCGGGGCGGAGCAGCACT 270
DB 793 CGCGAGATCTACACCAACCCCTGTGTGGAGAACTTGACGGGAGTTCCCGGCGAGCCG 852
QY 271 GGAGGAGCGCGCGCGGTGGCGGAGCGGCGGAGCAGCAGTGGCAGCAATCCAGC 330
DB 853 CAGGGCATCGAGGGGAGCATCCGACAGCCCGCCAGCTGATGAGACATCTGAACAGCATCAC 912
QY 331 AAAAGAAAAAACCAACATCGCTACAGCTGGGCGCACCGCGCGCGCTGTGAAAG 390
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QY 391 CGCAAGCGCTCAGCGACTACCGCTCTATCTGGCATGTTCGGGATCGGTGATGTC 450
DB 973 CCCGTGGCTTCAGCGCGCCCGAGTTACCTTCCCTGTACGCGACATGGGCAAGCC 1032

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Job time: 8061 sec

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Tue May 15 08:41:31 2001

us-09-254-590-21.rng

Page 1

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: May 14, 2001, 23:36:19 ; Search time 93.06 Seconds
(without alignments)
10915.318 Million cell updates/sec

Title: US-09-254-590-21
Sequence: 1 ATGAGCAGCTGCTGATACCA.....CTTCATCAGAGTACCTAG 1740

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Gapop 10.0, Gapext 1.0

Searched: 678276 seqs, 291890651 residues
Total number of hits satisfying chosen parameters: 1356552

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1740	100.0	1740	19 V35457	Human hsk2 coding
2	1487.2	85.5	1740	19 V35456	Rat RSK2 coding se
3	800.6	46.0	2224	19 V35472	Rat RSK3 coding se
4	796.4	45.8	1659	19 V35447	Rat truncated RSK3
5	778.4	44.7	1674	19 V35458	Truncated human hs
6	778.4	44.7	2462	19 V35473	Human hsk3 coding
7	778.4	44.7	2521	20 X08414	Human small conduc
8	666.8	38.3	1683	19 V35445	Human hsk1 coding
9	647.6	37.2	1374	19 V35446	Rat RSK1 coding se
10	485	27.9	1424	21 Z51630	Human membrane cha
11	423.8	24.4	1099	20 X00627	Human secreted pro

12	423.2	24.3	1080	20 X00703	Human secreted pro
13	241.8	13.9	1284	20 X83631	Human IKKα encodin
14	241.8	13.9	2238	20 X24826	Calcium activated
15	241.8	13.9	2261	20 X24825	Human calcium acti
16	240	13.8	1381	20 X24831	Mouse calcium acti
17	224	12.9	1287	19 V35463	Human hsk1 coding
18	193.8	11.1	1624	20 X24828	Calcium activated
19	162.6	9.3	1486	19 V59523	Human secreted pro
20	161.8	9.3	1354	19 V59505	Human secreted pro
21	161.8	9.3	1250	20 X24827	Calcium activated
22	147.8	8.5	1877	21 Z51619	Human membrane cha
23	147.8	8.5	293	14 Q59152	Human brain expres
24	145.8	8.4	293	14 Q39740	Expressed sequence
25	61.2	3.5	12588	15 Q63293	Sequence encoding
26	53.8	3.1	1272	20 X09010	Brn-3a polynucleot
27	53.8	3.1	1272	21 A29006	Human transcriptio
28	53.8	3.1	4524	20 V33912	Nucleotide sequenc
29	50.6	2.9	1266	20 X09011	Brn-3a polynucleot
30	50.6	2.9	1266	21 A29007	CDNA of the M3/6 g
31	50	2.9	2453	18 T86758	Small conductance
32	49.6	2.9	269	20 X08415	Plasmidum falcipla
33	49.4	2.8	2091	19 V59703	Human secreted pro
34	48.2	2.8	847	19 Q12007	Type/N-terminal do
35	48.2	2.8	1731	12 Q12007	CDNA of the M3/6 g
36	48.2	2.8	2415	18 T86757	Human androgen rec
37	48.2	2.8	3569	10 N91772	Androgen receptor
38	48.2	2.8	3569	18 T63407	Human androgen rec
39	48.2	2.8	3715	20 Z23424	DNA encoding angio
40	48.2	2.8	6463	21 Z45239	HIV codon altered
41	47.8	2.7	567	21 A29550	Full-length human
42	47.6	2.7	1731	12 Q12007	Human androgen rec
43	47.6	2.7	3715	12 Q12001	Full-length human
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45	46.6	2.7	3715	12 Q12001	Full-length human

ALIGNMENTS

RESULT 1	
V35457	V35457 standard; cDNA; 1740 BP.
AC	V35457:
XX	
XX	01-OCT-1998 (first entry)
DE	Human hsk2 coding sequence.
XX	
XX	Small conductance calcium-activated potassium channel protein 2;
KW	hsk2; human; potassium ion flux; ss.
KW	
XX	
OS	Homo sapiens.
XX	
PN	W09811139-A1.
PD	19-MAR-1998.
XX	
FE	10-SEP-1997; 97WO-US16033.
XX	
PR	17-APR-1997; 97US-0045233.
PR	11-SEP-1996; 96US-0026451.
PR	07-MAR-1997; 97US-0040052.
XX	
PA	(ICAG-) ICAGEN INC.
PA	(UYOR-) UNIV OREGON HEALTH SCI.
XX	
XX	Adelman JP, Bond CT, Maylie J, Silvia CP;
DR	WPI: 1998-207332/18.
DR	P-PSDB; W63707.
XX	
PT	DNA encoding calcium-activated potassium channel - useful in assays

potassium channel, whereas the human small conductance calcium-activated potassium channel protein 2 (hSK2) of the invention. The proteins of the invention are dimers of a calcium-activated potassium channel, where the monomer: (i) has a calculated molecular weight of between 40 and 80 kDa, and (ii) has a unit conductance of between 2 and 60 pS when the monomer is in the functional polymeric form of a potassium chain and is expressed in a *Xenopus* oocyte. Antibodies specific for the protein, and probes specific for the DNA can be used to detect the presence of the protein or DNA sequences in a sample. Host cells expressing the protein can be used in assays to identify compounds which increase or decrease the potassium ion flux through the protein. The transfected host cell can also be used for the recombinant production of the protein. The DNA sequences can also be used for the determinate mutations in the SK and IK genes in a computer system. The proteins encoded by the SK and IK genes can be used in a computer system for determining their three dimensional structure, which is useful for determining ligands that bind to the proteins.

Sequence 1740 BP; 473 A; 432 C; 435 G; 400 T; 0 other;

Query Match	100.0%;	Score 1740;	DB 19;	Length 1740;
Best Local Similarity	100.0%;	Pred. No. 0;		
Matches 1740; Conservative	0;	Mismatches	0;	

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QY	661	ATACGTGTGTGTGTATATATCCCATCTCTGGAAATTATATACATTACATGAGCGCCG	720
Db	661	atactggtgtgtgtatatacccatctctggaaattataatacttacaatgagcgccg	720
QY	721	CTTGCGCTCTCTATGCGCCATCCACAAACCGCGTATGTGSAATATATTTTATCTATA	780
Db	721	cttgccctctctatgcccacaaacacacgcgctgtgtgatatatttctacata	780
QY	781	CCAAATGTTCTTAAGACTCTATCTGATGATGGCAGAGTCATGCTTTTAACTAGCAACTTTTC	840
Db	781	ccaaatgtcttaagactctatctatctgttcgcagagcaagctttaaataagaaactttc	840
QY	841	ACTGATGCTTCCTCTAGGAAGATTGGAGCACTTAATAAGATAAACTTACATACAGTTTTT	900
Db	841	actgattgcttccctctagaagaatctgagcaactaataagaataacttcaatacagttt	900
QY	901	GTTATGAAGACTTTTAATGACTATATATGCCAGCACTACTCTGTGTTTAACTACTCA	960
Db	901	gttactgaagactttaatgactatataatgccagcaactactctgtttaaacttcaatac	960
QY	961	TTATGATATATTCGCCGATGCTGTCGAGAGTTGTAAAGTACCATGATCAACAGAT	1020
Db	961	ttatgatatatttcgccgatgctgtcgcagagttgtaaagtaccatgatcaacagat	1020
QY	1021	GTTACTAGCAACTTCCTTTGGAGCAGATGTGTGTTATCAATTAATTTCTCTCATTTGAT	1080
Db	1021	gttactagcaacttccctcttggagcagatgtgtgttatacaataacttctctccattg	1080
QY	1081	TATGTGACATGTACTTAACATATCTGTGAAAAGAGTGTGGTTATCTACTGTAAT	1140
Db	1081	tatgtgacatgttacttaaacatatctgtgaaaagagtctgacttaacttaccagaa	1140
QY	1141	ATGSGTGTGTTGCACAGCCCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	1200
Db	1141	atgsgtgtgtgtgtgcacagccctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt	1200
QY	1201	AAAGCAGAAAACACGTCGACAAATTTATATGTGATACTGACTGATAAAGACTATAA	1260
Db	1201	aaagcagaaaacacgtgcacaatttcaatgtatctcagctgactaaagagtataa	1260
QY	1261	AATGAGCTGCTCAATCTACTAGSAAACATGGCTAATTTTCAAAAATCAAGTGTATG	1320
Db	1261	aatgagctgctcaatctactagaaaacatggctaatTTTCAAAAATCAAGTGTATG	1320
QY	1321	AAAAAGTAGATCATGCAAAAAGTAAGAAAACATCAGCAAAAATTCCTGCATTAATCAT	1380
Db	1321	aaaaagtagatcatgcaaaaagtaagaaaacatcagcaaaaatTCCTGCATTAATCAT	1380
QY	1381	CAATTAAAGAGTAAAAATGSAACAGAGAACTGAATCACCAGCAAAACACTTTGGTG	1440
Db	1381	caattaaagagttaaaaaatgaaacagagaaactgaaatgacaaacaaacttggtg	1440
QY	1441	GACTTGGCAAAACCCAGAACATCATGTATGATATGATTTCTGATCTTAAGAAAGAT	1500
Db	1441	gacttggcaaaacccagaaacatcatgtatgatatgtatttctgacttaaaagaagaat	1500
QY	1501	GAAAGCTTGACAGAGAGATTGTTTACCTGTGAAAACAAAATTTGAGAACTTGATTTG	1560
Db	1501	gaagacttgcagagagattgtttacccgtgaaaacaaaattggaacttgaattgtagc	1560
QY	1561	ATCCAGCGCTCCTCGGGCTCAATAAGCCAGACCATATAGGCACAGCAGAGATTTCAAT	1620
Db	1561	atccagcgctcctctgggctcaataagccagacatcaagtcagcagcagagatllaatt	1620
QY	1621	GAGGCTCAGATGAGAGACTACAGCAAGCAGCTCACTTCAATGCTGAGCGCTCCGGTCC	1680
Db	1621	gaggctcagatgagagactacagcaagcagactcaacttcaaatgtgagcgctccggtcc	1680
QY	1681	TGCTCAGAGAGCGGGGCTCTTTCCACAGCAACCAATTCATCACAAGATAGCTAG	1740
Db	1681	tcgtcagagagcgcggtctcttccagagcacaacaactcatcagagagtagtag	1740

1189 aactaacttaccaaaacadaaagcatgtgcacaatttcattgatgtgatactacgctg

	RESULT	3	
V35472	ID	V35472 standard; cDNA; 2224 BP.	
XX	AC	V35472;	
XX	DT	01-OCT-1998 (first entry)	
XX	DE	Rat RSK3 coding sequence.	
XX	KW	Small conductance calcium-activated potassium channel protein 3.	
XX	KM	RSK3; rat; potassium ion flux; ss.	
XX	OS	Rattus sp.	
XX	FH	Key	
FT	CDS	Location/Qualifiers	
FT		2..2200	
XX		/tag= a	
PN		W09811139-A1.	
XX		.	
PD		19-MAR-1998.	
XX	PF	10-SEP-1997; 97WO-USI6033.	
XX	PR	17-APR-1997; 97US-0045233.	
PR		11-SEP-1996; 96US-0026451.	
PR		07-MAR-1997; 97US-0040052.	
XX	PA	(ICAG-) ICAGEN INC.	
PA		(UYOR-) UNTV OREGON HEALTH SCI.	
XX	PI	Adelman JP, Bond CT, Maylie J, Silvia CP;	
XX		WPI: 1998-207332/18.	
OR			

DR P-PSDB, W63715.
XX
XX DNA encoding calcium-activated potassium channel - useful in assays
PT to identify compounds which increase or decrease potassium Ion Flux
PT
XX
XX
XX
XX Claim 3; Page 123-124; 151pp; English.

This sequence encodes the rat small conductance calcium-activated potassium channel protein 3 (RSK3) of the invention. The proteins of the invention are monomers of a calcium-activated potassium channel, where the monomer: (1) has a calculated molecular weight of between 40 and 80 kDa; and (11) has a unit conductance of between 2 and 60 pS when the monomer is in the functional polymeric form of a potassium chain and is expressed in a *Xenopus* oocyte. Antibodies specific for the protein, and probes specific for the DNA can be used to detect the presence of the protein or DNA sequences in a sample. Host cells expression of the protein can be used in assays to identify compounds which increase or decrease the potassium ion flux through the protein. The transfected host cell can also be used in assays to determine production of the protein. The DNA sequences can also be used for determining mutations in the SK and IK genes in a computer system. The proteins encoded by the SK and IK genes can be used in a computer system for determining their three dimensional structure, which is useful for determining ligands that bind to the proteins.

Sequence 2224 BP; 531 A; 711 C; 537 G; 445 T; 0 other.

sequence 2224 BP; 531 A; 711 C; 537 G; 445 T; 0 other;

Query Match	Score	DB	Length
Best Local Similarity	800.6;	19;	2224;
72.1%;	Pred. No. 1	2e-106;	

Matches 1043; Conservative 0; Mismatches 404; Indels 0; Gaps 0;

[illegible]


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QY 648 CATCTCTTGGAAATAGTGTGTGCTATTCATCCACTGCGAATTAATACATTAC 707
DB 573 cactaagccggagatgctggtgctgacatccacccattcctggagagatcctt 632
QY 708 ATGAGAGCCCGGCTGCTTCTCATGTCCTCCCATCCAAACACCGCTGATGATAT 767
DB 633 ctgagcggacgcttgccttccctacacccctcggcagagcgagcgtgagacat 692
QY 768 TATTATCTATACCAATGTTCTTAAGACTCTATCTGATGCGAGTCACTCTTTACA 827
DB 693 tattctgctacatcccatgcttctgacctataccctgctgcgcgagctacgtctaa 752
QY 828 TAGCAAACTTTTACATGATGCCCTCTAGAAAGATGGAGCATGGAGTAAATGA 887
DB 753 tagcaagctcttcacggaatgctctcccgagacatcggggccctcaacagatcaact 812
QY 888 CAATACAGCTTTTGTATGAAAGCTTTAATGACTATATGCGCAGAACTGACTTGT 947
DB 813 caacacccgattcgtcagagacgtcactacatctgcccggcagcggtgctgctaat 872
QY 948 TTTTATATCTCATTTATGATGATAATTGCCGATGAGTGTCCGAGCTGTGAAGTAC 1007
DB 873 gtccagcatctctctggtatcatcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtc 932
QY 1008 TGATCAACAGAGTGTACTACGAACTCTCTTGGAGCGATGCTGTTGATATCAATTA 1067
DB 933 tgacacagagagcgtaactagtaactctggtggtcgtcgtcgtcgtcgtcgtcgt 992
QY 1068 TCTTCATCTTGTATGATGATGATGATGATGATGATGATGATGATGATGATG 1127
DB 993 ccttccatctggtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtc 1052
QY 1128 ACTTACGAAATTTATGAGTGTGCTGCTGACAGCCGCTGCTGATGATGATGATG 1187
DB 1053 tctactggtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgt 1112
QY 1188 GCTAGAACTTACCAAGCAGAAACACGTCACAAATTTGATGATGATGATGATG 1247
DB 1113 gctcgaactcaccacagacagacagacagacagacagacagacagacagacag 1172
QY 1248 TAAAGAGTAAATAATGCGCATGATGATGATGATGATGATGATGATGATGATG 1307
DB 1173 caacgagatcaagaagcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgt 1232
QY 1308 TACAAAGCTAGTCAAAAGATGATGATGATGATGATGATGATGATGATGATG 1367
DB 1233 cacaagcgtcctaagaagatctgacacgacacagacagacagacagacagac 1292
QY 1368 GCAAGCTATTCATCAATTAAGAACTGTAATAATGCAAGAGAACTGTAGACAC 1427
DB 1293 ccaagctattccacacacagcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgt 1352
QY 1428 AAGAACTTTGCTGAGCTTGGCAAGACCCAGCAATCATGATGATGATGATGATG 1487
DB 1353 caaacccctggtgagcccttccaaagatgagacagcgtcgtcgtcgtcgtcgt 1412
QY 1488 AAGCAAGAGAGTGAAGACTTGGAGAGAGATTTGTTACCTGGAAACAAATTTGA 1547
DB 1413 caaagacccgagtgagagacgtgagaaagcagcttgagacgtcgtcgtcgtcgt 1472
QY 1548 TTTGATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1607
DB 1473 ccttaacagcagcttcaatctccctggtcgtcgtcgtcgtcgtcgtcgtcgtcgt 1532
QY 1608 GAGAGATTTTATGAGCTGAGATGAGAGATGAGAGATGAGAGATGAGAGATG 1667
DB 1533 gtagcagcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgt 1592
QY 1668 GCGGTCCGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1709
DB 1593 ccaagcctcctcctcctcctcctcctcctcctcctcctcctcctcctcctc 1634

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RESULT 5
V35458
ID V35458 standard; cDNA, 1674 BP.
XX
AC V35458;
XX
DT 01-OCT-1998 (first entry)
XX
DE Truncated human hsk3 coding sequence.
XX
KW Small conductance calcium-activated potassium channel protein 3;
KW hsk3; human; potassium ion flux; ss.
XX
OS Homo sapiens.
XX
PN W0981139-A1.
PD 19-MAR-1998.
XX
PE 10-SEP-1997; 97MO-US16033.
XX
PR 17-APR-1997; 97US-0045233.
PR 11-SEP-1996; 96US-0026451.
PR 07-MAR-1997; 97US-0040052.
XX
PA (ICAG-) ICAGEN INC.
PA (UYOR-) UNIV OREGON HEALTH SCI.
XX
PI Adelman JP, Bond CT, Maylie J, Silvia CP.
XX
DR WPT: 1998-207332/18.
XX
P-PSDB: W63708.
XX
PT DNA encoding calcium-activated potassium channel - useful in assays
XX to identify compounds which increase or decrease potassium ion flux
XX
PS Claim 3; Page 112; 151pp; English.
XX
CC This sequence encodes the human small conductance calcium-activated
CC potassium channel protein 3 (hsk3) of the invention. The proteins of the
CC invention are monomers of a calcium-activated potassium channel, where
CC the monomer: (i) has a calculated molecular weight of between 40 and
CC 80 kDa; and (ii) has a unit conductance of between 2 and 60 pS when the
CC monomer is in the functional polymeric form of a potassium channel and is
CC expressed in a Xenopus oocyte. Antibodies specific for the protein, and
CC probes specific for the DNA can be used to detect the presence of the
CC protein or DNA sequences in a sample. Host cells expression of the
CC protein can be used in assays to identify compounds which increase or
CC decrease the potassium ion flux through the protein. The transfected host
CC cell can also be used for the recombinant production of the protein. The
CC DNA sequences can also be used for determine mutations in the SK and IK
CC genes in a computer system. The proteins encoded by the SK and IK genes
CC can be used in a computer system for determining their three dimensional
CC structure, which is useful for determining ligands that bind to the
CC proteins.
XX
SQ Sequence 1674 BP; 392 A; 521 C; 409 G; 352 T; 0 other;

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Query Match 44.7%; Score 778.4; DB 19; Length 1674;
Best Local Similarity 73.6%; Pred. No. 5,5e-191;
Matches 992; Conservative 0; Mismatches 356; Indels 0; Gaps 0;

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QY 288 TGGCGGAGACGGGACGACGACGACGACGACGACGACGACGACGACGACGACG 347
DB 213 TCGCGGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGAC 272
QY 348 CATGCGCTACAGCTGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 407
DB 273 catggtctataagctggtgacacagagagcgtcttggaaagagaaagcgactgag 332
QY 408 CTACGCGCTCATCTTGGGCAATGTTGGGCAATGTTGGGCAATGTTGGGCAATGTT 467

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Db 333 ctatgctcgtatcttggagatgctgtaagtgatgagacgagctctc 392
 Qy 468 GTGGGGGCGCTACGACAAAGCGCTCGCTATTCCTTACCTTAAATGGCTTATCAGTCT 527
 Db 393 ttgggttgtaactcaagagactccatgcttctcgttgcctcctaagtgcttcatcagct 452
 Qy 528 CTCACGATCATCCGCTCGCTCGATCCGTGATACACGCCAGGGAATACAGTGT 587
 Db 453 gtccacatcatccttctggcttgatcaccgccaacgaagtgatccatcctc 512
 Qy 588 CATGTGGACAAATGAGCAGATGAGTGAATAGCCATGATGATGATGATGATGAT 647
 Db 513 cgtatgacgaacgagcgagctgagctgagctgagctgagctgagctgagctgagct 572
 Qy 648 CATCTGTTGGAATATCTGCTGCTGATATCATCCCTTACCTGGAATATATCATTCAC 707
 Db 573 catcagcttgagatgctgagctgagctgagctgagctgagctgagctgagctgagct 632
 Qy 708 ATGAGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 767
 Db 633 ctgagcgagcagcgctgagctgagctgagctgagctgagctgagctgagctgagct 692
 Qy 768 TATTTTATCTATACCAATGCTTCTTAAGCTATCTGATGCTGCAAGTATGCTTTACA 827
 Db 693 catcctgctatcccatcctcctgagctgagctgagctgagctgagctgagctgagct 752
 Qy 828 TAGCAAACTTTTCACTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 887
 Db 753 cagcagctcctcctcagctgagctgagctgagctgagctgagctgagctgagctgagct 812
 Qy 888 CATATACAGCTTTGTTATGAGAACTTAAATGATATGCTGAGAACTGCTGCTGCT 947
 Db 813 caaaccccgcttgcataagacgctgagctgagctgagctgagctgagctgagctgagct 872
 Qy 948 TTTTATGATCTCATATGATATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1007
 Db 873 gtacagctcctcctcgtgagctgagctgagctgagctgagctgagctgagctgagct 932
 Qy 1008 TGAACAAAGAGTATGATGATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1067
 Db 933 tgaccagagagctgagctgagctgagctgagctgagctgagctgagctgagctgagct 992
 Qy 1068 TCTCTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1127
 Db 993 ccttccatgctgagctgagctgagctgagctgagctgagctgagctgagctgagct 1052
 Qy 1128 ACTTACGGAATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1187
 Db 1053 cctcagctgagctgagctgagctgagctgagctgagctgagctgagctgagctgagct 1112
 Qy 1188 GCTAGAACCTTACCAAGAGAGAAACACGCTGACAAATTTATGATGATGATGATGATGAT 1247
 Db 1113 gctggaactcaccagcgagagacgagctgagctgagctgagctgagctgagctgagct 1172
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 Qy 1308 TACAAAGCTAGTGAAGAGTATGATGATGATGATGATGATGATGATGATGATGATGAT 1367
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 Qy 1368 GCAAGCTATTCATATTAAGAGTGAAGAGTGAAGAGTGAAGAGTGAAGAGTGAAGAGTGA 1427
 Db 1293 ccaagctatccacagctgagctgagctgagctgagctgagctgagctgagctgagctgagct 1352
 Qy 1428 AAACACTTTGCTGAGCTTGGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1487
 Db 1353 caaacctctgagctgagctgagctgagctgagctgagctgagctgagctgagctgagct 1412
 Qy 1488 AAACGAAG 1547

Db 1413 caatgacgagcgagagacacctgagagagagagagagagagagagagagagagagagag 1472
 Qy 1548 TTTGATTTGTTATACATCCACAGCCCTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1607
 Db 1473 tctcagcagagctcactccctcctgagctgagctgagctgagctgagctgagctgagct 1532
 Qy 1608 GAGAGATTTTATGAGAGCTGAGATGAGAG 1635
 Db 1533 gcagcagctcctcctgagctgagctgagctgagctgagctgagctgagctgagct 1560
 RESULT 6
 ID V35473 standard; cDNA; 2462 BP.
 XX V35473;
 AC V35473;
 DT 01-OCT-1998 (first entry)
 XX Human hSK3 coding sequence.
 DE Small conductance calcium-activated potassium channel protein 3;
 KW hSK3; human; potassium ion flux; ss.
 XX Homo sapiens.
 OS
 FH Key Location/Qualifiers
 FT CDS 252..2462
 FT /*tag= a
 PN W09811339-A1.
 PD 19-MAR-1998.
 XX 10-SEP-1997; 97WO-US16033.
 PF 17-APR-1997; 97US-0045233.
 PR 11-SEP-1996; 96US-0026451.
 PR 07-MAR-1997; 97US-0040052.
 XX
 PA (ICAGEN) ICAGEN INC.
 PA (UYOR-) UNIV OREGON HEALTH SCI.
 PI Adelman JP, Bond CT, Maylie J, Silvia CP;
 XX WPI: 1998-207332/18.
 DR P-PSDB: W63717.
 XX
 PT DNA encoding calcium-activated potassium channel - useful in assays
 PT to identify compounds which increase or decrease potassium ion flux
 PS Claim 3; Page 128-129; 151pp; English.
 XX
 CC This sequence encodes the human small conductance calcium-activated
 CC potassium channel protein 3 (hSK3) of the invention. The proteins of the
 CC invention are monomers of a calcium-activated potassium channel, where
 CC the monomer: (i) has a calculated molecular weight of between 40 and
 CC 80 kDa; and (ii) has a unit conductance of between 2 and 60 pS when the
 CC monomer is in the functional polymeric form of a potassium chain and is
 CC expressed in a Xenopus oocyte. Antibodies specific for the protein, and
 CC probes specific for the DNA can be used to detect the presence of the
 CC protein or DNA sequences in a sample. Host cells expression of the
 CC protein can be used in assays to identify compounds which increase or
 CC decrease the potassium ion flux through the protein. The transfected host
 CC cell can also be used for the recombinant production of the protein. The
 CC DNA sequences can also be used for determine mutations in the SK and IK
 CC genes in a computer system. The proteins encoded by the SK and IK genes
 CC can be used in a computer system for determining their three dimensional
 CC structure, which is useful for determining ligands that bind to the
 CC proteins.
 CC
 XX Sequence 2462 BP; 552 A; 814 C; 617 G; 479 T; 0 other;
 SQ

[illegible]

OY	1308	TACAAAGCTATGTGAAAAATGATGATCTGTGAAAAAGCTAAAGAAAAATCAACGAAAAATTCCT	1367
Db	2021	caacaagctctaagaagatctgcctctgccaagctggaagaacaccagggaaagttccct	2080
OY	1368	GCAACACTTTCATCAATTAGAGCTGTAAAAATGCAACAGAGAAACTGAATGACCAAGC	1427
Db	2081	ccaagctatccaccagcttggaggagcttcaagactggaacagaaggaaagctggagctgacaaagc	2144
OY	1428	AACACACTTGGTGGCATTTGGCAAAAGCACCAGAAACATCATGATGATGATGATTTGTGCATT	1487
Db	2144	caacactctggttggaacctcttccaagatgccaagaatgtaactgtatgaacttaatacaagaact	2200
OY	1488	AACCAAAAGAGTGAAGACTTCGAGAAAGAGATTCTTACCTTGGAAACAAAATTTAGAGAC	1547
Db	2201	caatgacaggagagaaagaaactctggaagaagacagatctggaagctctggagctcggagagca	2260
OY	1548	TTTGTATGTGGATGATCCACAGCCCTCCCTGGGCTGCTAAAGCAACATTCACAGCAGACGA	1607
Db	2261	ttctaccgcgaagcttcaactcctctgcgcgtgtatctatccgcgaataccctgcgcgcgaagca	2320
OY	1608	GAGAGATTTTCATTGAGAGCTCAAGATGAGAG	1635
Db	2321	gcagcagctctctgtctgcacatcatcagag	2348

```

RESULT 7
X08414
ID X08414 standard; cDNA; 2521 BP.
XX
AC X08414;
XX
DT 28-JUN-1999 (first entry)
XX
DE Human small conductance calcium activated potassium channel gene.
XX
KW Human small conductance calcium activated potassium channel;
KW hKCa3/KCNN3; bipolar disease; schizophrenia; treatment; diagnosis;
KW detection; transgenic animal; gene therapy;
KW neuropsychiatric disorder; neurological disorder;
KW neuromuscular disorder; immunological disorder; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FH CDS 287..2482
FT /*tag= a
FT /product= "Small conductance calcium activated
FT polyA_signal potassium channel polypeptide"
FT /*tag= b
FT /label= Poly-A signal
FT polyA_site 2509..2521
FT /*tag= c
FT /label= Poly-A region
XX
PN WO9903889-A1.
XX
PD 28-JAN-1999.
XX
PE 14-JUL-1998; 98WO-US14902.
XX
PR 08-JAN-1998; 98US-0070741.
PR 15-JUL-1997; 97US-0052556.
XX
XX (REGC ) UNIV CALIFORNIA.
XX
PA
XX
PI Chandu KG, Fantino E, Gargus JJ, Gutman G, Kalman K;
XX
DR WPI: 1999-132165/11.
DR P-PDB: W96312.
XX
PT New human small conductance calcium activated potassium channel-3 -
PT useful for diagnosis, treatment and prevention of particularly

```

PR 11-SEP-1996; 96US-0026451.

QY	756	TGATGTGATATTATTTTATATCTATACAGAGTCTTAAAGACTCTATACATGATGACCAAGC	815
Db	426	gagatgcatgagcttccctgtccatcccaatgcttctgcgctccctacatccctgctgagct	485
QY	816	CATGCTTTTACATGCAAAACTTTTGCATGATGCGCTCCTCTAGAAAGCATTTGGACACTTAA	875
Db	486	catgctctccgaacagccgacatcttccagagcagcatccagctcgacagatccggagccctgaa	545
QY	876	TAAATTAACCTTCATATACAGCTTTTGTTATATGAAGCTTTAATGACATATGAGCCAGCAAC	935
Db	546	ccgctgtacatcttcaacacacgccttgcacccaagaacacatcatgacatctgcctgcgcgac	605
QY	936	TGTACTCTTGGTTTTAGTATCTCATTTATGAGTAATTTGCCGATGACGTGTCCAGCTTG	995
Db	606	cgctgctgttgcttccacgacatccctccctgtgatactgcgtatgacatgacagctgcgcgtg	665
QY	996	TGAAGGTACCATGATGATCAAGAGAGATTTATATGAGCACTTCCTGTGAGACGATGTGGTTGAT	1055
Db	666	tgaagagtgaccatgataaacaacggaaagtgacacgaacatcttcctgggggcagctggtcat	725
QY	1056	ATCATTAACCTTTTCTCTCCATTGGTTATGATGATGATGATGATCTTAACATACACTGTGAGAA	1115
Db	726	ctccatctacatcttccctgtccatccgcgcagcggaatgctgtgcgcacacccactcgtggaa	785
QY	1116	AGGATCTCGCTTACTTACGGAATTTATGGTGTGCTGTGCACAGCCCTGGTGTGATGCT	1175
Db	786	gggcgtgtgtctcgtccacacggacatcatgtggagcagcgtgtgaactgcgtgtgttgccgt	845
QY	1176	AGTGGCAAGNAGATCTGAAACTTACCAAGCAGAGAAAACGTGCGACATTTTCATATATGA	1235
Db	846	ctgtgcgcgcgaagcttggaaactccacacgaagctgtgagaacaacgtgcacacttcatgtgag	905
QY	1236	TACTCAGCTGACTTAAAGATGTAATAAATGCTACGCTGCCAATGTACTCAAGGAAACATGGCT	1295
Db	906	cacacagctccacacagcgggtttaaaaaocgcgtgcgaacgcttccagggagacatgct	965
QY	1296	AATTTACAAAATATACAAAGCTTAGTGAAAAAGATAGATCATGCAAAAATGAAAGAAATCA	1355
Db	966	catctcaaaaacaacacagccttagtgaagaagccagaccacaaagccgggtctcgaaacaca	1025
QY	1356	ACGAAATATTCCTCGAAGCTATTCATTCAT-----TAGAAGTGTAAAAATGAGACA	1406
Db	1026	gcgttaagttcttcttaaggccaatccatccagggcagaagagctccggaactgtgaagattga	1085
QY	1407	GAGGAATATGATGATCCAGCAAAACCTTTGGTGGACTTGGCAAGACCCGGAACATTCAT	1466
Db	1086	agggaaagtgatgatcatgaagcaaacacgcgtgcgtaccctggcacaagacacagagctgc	1145
QY	1467	GTAATGATGATGATTTCTGACTTAAACGAAGAAGATGAAAGCTTGAGAGAGATTTGTTAC	1526
Db	1146	ataatgagtggtgtgcggagctgcagggccacagagaagatgtgaaagcccgctctggtctgc	1205
QY	1527	CTGTGAAACAAAATTTAATAGACTTTTATTTGGTATGACATCCAGCGCCCTCGCTGGAGCTCAATAG	1586
Db	1206	ctgtgagaagccgcctgtgaatgtctctagggccctccctcgaagccctatccaaagtccataagc	1265
QY	1587	CCAGACCATCAGGC 1600	
Db	1266	ccaagccatattgcc 1279	
RESULT	10		
Z51630		Z51630 standard; cDNA; 1424 BP.	
XX			
AC			
XX	Z51630:		
XX			
DT	21-JUN-2000	(first entry)	
XX			
DE	Human membrane channel protein-14 (MECHP-14)	cDNA.	
XX			
KW	Membrane channel protein-14; MECHP-14; diagnosis; treatment; Lymphoma;		

Query	March	Score	485	DB	21	Length	1424
Best Local Similarity	97.1%	Ped	No	2	5e-115		
Matches	494	Conservative	0	Mismatches	13	Indels	0
						Gaps	0
QY	1232	TGGATACAGTCAGTCAAAAGAGTAAAAATGACGTCGCAATGATCAGGAAACAT	1291				
Db	591	tcgcttgctgtgctccttaacagtgataaaatgacgtgcacatgcttcacagggaataac	650				

QY	1292	GGCTAATTTACAAAATTC	1351
Db	651	ggcctaattccaaaatacaataagctcagtgaaaaagatagatcctgcataaagttaagaaaac	710
QY	1352	ATCAACGAAAATTCCTGCACGCTATTTCATCAATTAAGAAGTGTAAATAATGCACAGCA	1411
Db	711	atcaacgaaaatctccctgcaaacctatcaatcaactaagaagtgttaaaaaatggagcagaagga	770
QY	1412	AACGTAATGACACAGCAACACTTTGGTGGACTTGGCAAGACCCGAAACATCATGTATG	1471
Db	771	aactgaatgacgaagaacaacaccttggctggacttggcacaagaaccaagaacatcatgtatg	830
QY	1472	AATGATATTTGTGACTTTAAACGAAGAAGTGAAGACTTCGAGAAAGAGATTGTTACCTTGG	1531
Db	831	ataatgattcttcgacttaaacgaagaagatgtaagactcctgagaagaagatgtttacacctgg	890
QY	1532	AAACGAATATAGAGACTTTGATTGGTAGAGATCCAGGCCCTCCCTGGGTCCATTAAGCCAGA	1591
Db	891	aaacaaactagagacttgattgtgtgagatccaccgcctccctctggagctcataaagaaccga	950
QY	1592	CCATCAGCAGCAGCAGCAGAGAGATTTATTGAGGCTCAGATGAGAGCGCTACGACACACAG	1651
Db	951	ccatcagcagcagcagcagcagagatllcatttgagctcagaatgtagagctcagaagaacacg	1010
QY	1652	TCACCTTACAAATCGATGAGGGGTCGCCGCTCTGTCACAGAGAGCGCGGGTCTCTTCCACAG	1711
Db	1011	tcaattcaaatcgtcagcggtcccgctcctctccagagagcggtgctctcttccaag	1070
QY	1712	CACCACCAACTTCATCATGACAGAGACTGAG	1740
Db	1071	caccaccaacttcattcatcagagatgactag	1099
RESULT	11		
XX00627			
ID	XX00627	standard; DNA; 1099 BP.	
XX			
AC	XX00627;		
XX			
DT	25-MAR-1999	(first entry)	
XX			
DE		Human secreted protein gene 17 clone HELB406.	
KM		Human; secreted protein; fusion protein; gene therapy; protein therapy;	
KM		diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia;	
KM		developmental abnormality; foetal deficiency; blood; allergy; renal; ds;	
KM		immune system; asthma; lymphocytic disease; brain; hepatic; lymphoma;	
KM		inflammation; ischaemic shock; Alzheimer's disease; restenosis; AIDS;	
KM		cognitive disorder; schizophrenia; prostate; obesity; osteoclasts; thymus;	
KM		osteoporosis; arthritis; testis; lung; thyroiditis; thyroid; digestion;	
KM		endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.	
OS		Homo sapiens.	
XX			
XX			
PN	W09842738-A1.		
XX			
PD	01-OCT-1998.		
XX			
PF	19-MAR-1998;	98WO-US05311.	
XX			
PR	30-MAY-1997;	97US-0050937.	
PR	21-MAR-1997;	97US-0041276.	
PR	21-MAR-1997;	97US-0041277.	
PR	21-MAR-1997;	97US-0041281.	
PR	30-MAY-1997;	97US-0042344.	
PR	30-MAY-1997;	97US-0048069.	
PR	30-MAY-1997;	97US-0048094.	
PR	30-MAY-1997;	97US-0048095.	
PR	30-MAY-1997;	97US-0048096.	
PR	30-MAY-1997;	97US-0048099.	
PR	30-MAY-1997;	97US-0048131.	
PR	30-MAY-1997;	97US-0048135.	

PR 30-MAY-1997; 9705-0048154.
 PR 30-MAY-1997; 9705-0048160.
 PR 30-MAY-1997; 9705-0048186.
 PR 30-MAY-1997; 9705-0048187.
 PR 30-MAY-1997; 9705-0048188.
 PR 30-MAY-1997; 9705-0048350.
 PR 30-MAY-1997; 9705-0048351.
 PR 30-MAY-1997; 9705-0048352.
 PR 30-MAY-1997; 9705-0048355.
 PR 05-AUG-1997; 9705-0054804.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 XX
 PI Brewer LA, Duan R, Edner R, Ferrie AM, Florence KA;
 PI Greene JM, Hu JS, Lafleur DW, Moore PA, Ni J, Olsen HS;
 PI Rosen CA, Ruben SM, Shi Y, Young P;
 XX
 DR WPI: 1999-070066/06.
 DR P-PSDB: W67823.
 XX
 PT New isolated human genes and the secreted polypeptides they encode -
 PT useful for diagnosis and treatment of e.g. cancers, neurological
 PT disorders, immune diseases, inflammation or blood disorders
 XX
 PS Claim 1: Page 183-184; 385pp; English.
 XX
 CC This sequence represents a nucleic acid molecule which encodes a secreted
 CC human protein. The gene number, and the clone it is derived from, are
 CC detailed in the descriptor line. The gene can be used to generate fusion
 CC proteins by linking to the gene to a human immunoglobulin Fc portion
 CC (e.g. X00602) for increasing the stability of the fused protein as
 CC compared to the human protein only.
 CC The invention relates to 87 novel genes and their fragments (nucleic acid
 CC sequences: X00611-X00724; amino acid sequences W67807-W68004) which
 CC are useful for preventing, treating or ameliorating medical conditions
 CC e.g. by protein or gene therapy. Also, pathological conditions can be
 CC diagnosed by determining the amount of the new polypeptides in a sample
 CC or by determining the presence of mutations in the new polynucleotides.
 CC Specific uses are described for each of the 87 polynucleotides, based on
 CC which tissues they are most highly expressed in (see X00611 for described
 CC uses).
 XX
 SQ Sequence 1099 BP; 276 A; 333 C; 257 G; 232 T; 1 other:
 XX
 Query Match 24.4%; Score 423.8; DB 20; Length 1099;
 Best Local Similarity 69.3%; Pred. No. 1.4e-99;
 Matches 645; Conservative 0; Mismatches 237; Indels 49; Gaps 3;
 QY 754 GCTGATGATGATATTTATTTATACCAATGTTCTTAAAGCTATATGATGGCAGA 813
 DB 8 gccgatlgygacatcatcctgtctatcccatgtctcgtcgttacctgtatgcgcga 67
 QY 814 GTCATGCTTTTACATACCAACCTTTTACCTGCTGCTGAGAGATGAGACACTT 873
 DB 68 gtacatgctgtcgc 127
 QY 874 AATAAGATAAATCTCAATACAGCTTTTGTATGAAGCTTTTATGACTATATGCCAGCA 933
 DB 128 aacaagatcaactcaacacccgcttgcatagaagcgtatgacatcatcctgtgc 187
 QY 934 ACTGACTCTGCTTTTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 993
 DB 188 actgactgctcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtc 247
 QY 994 TGTGAAA-----GGTACCAAT 1008
 DB 248 tgtgaaagtcctgaaatcaccagccagcctcgtcgtcgtcgtcgtcgtcgtcgtcgt 307
 QY 1009 GATCAGACAGATGTTTACTGACATGCTTCTGAGAGATGTTGTTGATATCAATAACTTTT 1068
 DB 308 gaccagcagagcgaactagtaacttctcgtggtgctgcatggtcgtcgtcgtcgtcgtc 367

QY 1069 CTCATCTGTTGTTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1128
 DB 368 ctctcatctgtctatcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgt 427
 QY 1129 CTTACTGGAATTTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1188
 DB 428 ctctactgcatcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgt 487
 QY 1189 CTGAACTTACCAAG 1248
 DB 488 ctggaactcacaagcggag 547
 QY 1249 AAAAGATGAAAAATGCACTGCTGCAATGATGATGATGATGATGATGATGATGATGAT 1308
 DB 548 aagagatcagaagatcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgt 607
 QY 1309 ACAAGCTAGTGTGAAAAAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1368
 DB 608 acaagctagtcgaagaagaatgacatgccaagaagagagagagagagagagagagagag 667
 QY 1369 CAAGCTATTCATCAATTTAAGAAGTG---TAAAAATGGAACAGAGAGAA-CTGAATGACCA 1424
 DB 668 ccaagctatccaccaggttgagagcgtcccaagatgagacagagagagagagagagagag 727
 QY 1425 AGCAAAACCTTTGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1484
 DB 728 agcaaacacctcgtggtgagacatcctcgaagatgagacagagagagagagagagagag 787
 QY 1485 CTTAAACGAAAGAGATGAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1544
 DB 788 actcaatgacag 847
 QY 1545 GACTTGTGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1604
 DB 848 gacttcaacgcagagatcctcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgt 907
 QY 1605 GCAGAGAGATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1635
 DB 908 gcagagagagatcctcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgt 938
 RESULT 12
 ID X00703 standard; DNA; 1080 BP.
 AC X00703;
 DT 25-MAR-1999 (first entry)
 XX
 DE Human secreted protein gene 17 clone HELBA06.
 XX
 KW Human; secreted protein; fusion protein; gene therapy; protein therapy;
 KW diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukemia;
 KW developmental abnormality; foetal deficiency; blood; allergy; renal; ds;
 KW immune system; asthma; lymphocytic disease; brain; hepatic; lymphoma;
 KW inflammation; ischaemic shock; Alzheimer's disease; restenosis; AIDS;
 KW cognitive disorder; schizophrenia; prostate; obesity; osteoclast; thymus;
 KW osteoporosis; arthritis; testis; lung; thyroiditis; thyroid; digestion;
 KW endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.
 OS Homo sapiens.
 PN WO9842738-A1.
 PD 01-OCT-1998.
 XX
 PE 19-MAR-1998; 98WO-US05311.
 XX
 PR 30-MAY-1997; 97US-0050937.
 PR 21-MAR-1997; 97US-0041276.
 PR 21-MAR-1997; 97US-0041277.
 PR 21-MAR-1997; 97US-0041281.
 PR 21-MAR-1997; 97US-0042344.

[illegible]

Claim 2"

FT XX
 XX MO9903882-A2.
 XX
 PD 28-JAN-1999.
 XX
 PF 13-JUL-1998; 98WO-GB02058.
 XX
 PR 09-OCT-1997; 97GB-0021366.
 PR 15-JUL-1997; 97GB-0014760.
 XX
 PA (ZENEC) ZENEC LTD.
 XX
 PI Aiyar J, Logsdon NJ;
 XX
 DR WPI: 1999-132158/11.
 DR P-PSDB: W98017.
 XX
 PT New isolated leukocyte calcium activated potassium channel nucleic
 PT acids - used to develop products for treating e.g. inflammation,
 PT asthma, allergies, graft rejection, proliferative disorders,
 PT neurodegenerative diseases or autoimmune diseases
 PS
 Claim 2; Page 97; 139pp; English.

XX
 CC This polynucleotide, the coding region of which is claimed, encodes
 CC a novel human calcium activated potassium channel (CaPC) designated
 CC hKCa4 (see W98017). This full-length cDNA was isolated from a
 CC human lymph node library using a probe derived from an EST sequence
 CC that was identified from a database search for novel potassium
 CC channels. The 2.2 kb clone is a 5'UTR variant of the sequence
 CC given in X24825. The novel hKCa4 gene maps to human chromosome
 CC 19q13.1. Transcripts are detected in placenta, prostate, thymus,
 CC spleen, colon and many cell lines of haematopoietic origin.
 CC Calmodulin is an interaction partner for hKCa4 and is possibly the
 CC calcium sensor. hKCa4 is expressed at a high level in activated
 CC T cells. The invention also provides expression vectors, antisense
 CC molecules, host cells, purified polypeptides and polynucleotides,
 CC antibodies and (anti)agonists of CaPC function. Compounds that
 CC modulate CaPC activity can be used in treating diseases which are
 CC manifested by dysfunctional leukocytes such as acute and chronic
 CC inflammation, asthma, allergies, graft rejection, proliferative
 CC disorders, anaemias, neurodegenerative diseases with immunological
 CC components, as well as autoimmune disease including rheumatoid
 CC arthritis, type-1 diabetes mellitus, multiple sclerosis, myasthenia
 CC gravis, systemic lupus erythematosus, Sjogren's syndrome, mixed
 CC connective tissue disease, and experimental allergic
 CC encephalomyelitis. The products can also be used for gene therapy,
 CC detection and diagnosis.

SO Sequence 2238 BP; 421 A; 666 C; 707 G; 444 T; 0 other:

Query Match 13.9%; Score 241.8; DB 20; Length 2238;
 Best Local Similarity 52.1%; Pred. No. 1.8e-52;

Matches 627; Conservative 0; Mismatches 552; Indels 24; Gaps 3;

QY 362 TGGGACACGGGGCCCTGTGTGAAAGCGAAGCGGCTCAGCACTACGGCTCATCT 421
 DB 411 tggagagccggaagagcgtctgagcagagagagagctctcggccgctggagacgtgggc 490
 QY 422 TCGGCATGTTGGCATCGTGTGATGATGAGACGAGCTGTGTGTGGGCGCTACG 481
 DB 491 tggcagaagactgcatgacatgctgcatgacagagatgctggttgcggggggt 550
 QY 482 ACAAGCGCTGCTGATTCCTTAAGCTGAAATGCTTATCACTCTCTCAAGATCATCC 541
 DB 551 gctcgtggcgctctacacctctccgtgtaaatgacagaccacatctccacctctac 610
 QY 542 TCGCTGGTGTGATCATGCTGTACACGACGAGGAATATGATTGTTTCATGTGACATG 601
 DB 611 tctctcctcctcgtgctcttctcctcctcctcctcctcctcctcctcctcctcctcctc 670

QY 602 GAGCAGATGACTGTGAGATAGATGACTTATGAGATATTTCTTCATCTGCTTGAAA 661
 DB 671 ggcctgagagactgagcgtgagcagcagcagcagcagcagcagcagcagcagcagcagc 730
 QY 662 TACTGTGTGTGTGATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTC 714
 DB 731 tggtagtgtagtgtagtgtagtgtagtgtagtgtagtgtagtgtagtgtagtgtagtgtag 790
 QY 715 -GCCCGGCTTGTCT 772
 DB 791 gggcgccgctgacctcccgagcagcagcagcagcagcagcagcagcagcagcagcagcagc 850
 QY 773 TATCATACCAATGTTCTTAAAGTATGATGATGATGATGATGATGATGATGATGATGAT 832
 DB 851 tggcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 910
 QY 833 AACTTTTCACTGATGCT 892
 DB 911 ggcctcctcctcctcctcctcctcctcctcctcctcctcctcctcctcctcctcctcctc 970
 QY 893 CACGTTTGTGATGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 952
 DB 971 actggttcgtgagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 1030
 QY 953 GTATTCATTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1012
 DB 1031 cgtctgagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 1089
 QY 1013 AACGAGATGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1072
 DB 1090 -aagtcacatgagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 1144
 QY 1073 CCATGTTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1132
 DB 1145 ccatcgtctatgtagtgtagtgtagtgtagtgtagtgtagtgtagtgtagtgtagtgtagtg 1204
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 DB 1205 ctgagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 1264
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 QY 1553 TTG 1555
 DB 1616 ctg 1618

RESULT 15
 X24825
 ID X24825 standard; cDNA: 2261 BP.
 XX

AC X24825;
 XX 21-JUN-1999 (first entry)
 XX Human calcium activated potassium channel hKCa4 full-length cDNA.
 XX
 KW Calcium activated potassium channel; hKCa4; human; leukocyte;
 KW T cell; T lymphocyte; inflammation; asthma; allergy;
 KW graft rejection; proliferative disorder; anaemia;
 KW neurodegenerative disease; autoimmune disease; multiple sclerosis;
 KW rheumatoid arthritis; diabetes mellitus; multiple sclerosis;
 KW myasthenia gravis; systemic lupus erythematosus;
 KW Sjogren's syndrome; mixed connective tissue disease;
 KW experimental allergic encephalomyelitis; diagnosis; therapy; ss.
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 OS Homo sapiens.
 FH
 FH Key Location/Qualifiers
 FT CDS 396..1679
 FT /tag= a
 FT /note= "this region is specifically claimed in
 FT Claim 2"
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 XX MO9903882-A2.
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 XX 28-JAN-1999.
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 XX 13-JUL-1998; 98MO-GB02058.
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 XX 09-OCT-1997; 97GB-0021366.
 XX 15-JUL-1997; 97GB-0014760.
 XX
 XX (ZENEC) ZENEC LTD.
 XX
 XX Aiyar J, Logsdon NJ;
 XX WPI; 1999-132158/11.
 XX P-PSDB; W98017.
 XX
 PT New isolated leukocyte calcium activated potassium channel nucleic
 PT acids - used to develop products for treating e.g. inflammation,
 PT asthma, allergies, graft rejection, proliferative disorders,
 PT neurodegenerative diseases or autoimmune diseases
 PT
 PS Claim 2; Page 86-86; 139pp; English.
 XX
 CC This polynucleotide, the coding region of which is claimed, encodes
 CC a novel human calcium activated potassium channel (CACP) designated
 CC hKCa4 (see W98017). This full-length cDNA was isolated from a
 CC human lymph node library. The novel gene maps to human chromosome
 CC 19q13.1-13.2. Transcripts are detected in placenta, prostate,
 CC thymus, spleen, colon and many cell lines of haematopoietic origin.
 CC Calmodulin is an interaction partner for hKCa4 and is possibly the
 CC calcium sensor. hKCa4 is expressed at a high level in activated
 CC T cells. The invention also provides expression vectors, antisense
 CC molecules, host cells, purified polypeptides and polynucleotides,
 CC antibodies and (ant)agonists of CACP function. Compounds that
 CC modulate CACP activity can be used in treating diseases which are
 CC manifested by dysfunctional leukocytes such as acute and chronic
 CC inflammation, asthma, allergies, graft rejection, proliferative
 CC disorders, anaemias, neurodegenerative diseases with immunological
 CC components, as well as autoimmune disease including rheumatoid
 CC arthritis, type-1 diabetes mellitus, multiple sclerosis, myasthenia
 CC gravis, systemic lupus erythematosus, Sjogren's syndrome, mixed
 CC connective tissue disease, and experimental allergic
 CC encephalomyelitis. The products can also be used for gene therapy,
 CC detection and diagnosis.
 CC
 XX Sequence 2261 BP; 446 A; 660 C; 707 G; 446 T; 2 other;
 SQ

Query Match 13.9%; Score 241.8; DB 20; Length 2261;
 Best Local Similarity 52.1%; Pred. No. 1.8e-52;

	Matches 627; Conservative 0; Mismatches 552; Indels 24; Gaps 3;
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QY 422	TGCGCATGTTGCGGATCGGTCATGGTATGATGAGACCGACCTGTGCGGCGCTTACG 481
DB 490	tgagcaggaactgcatctgactatgctgctgcatgacgaagatgctgctgagcagc
QY 482	ACAAAGCGTCGCTGATTCCTTAACTCTGAATGCTTATAGCTCTCCAGATATCC 541
DB 550	gctcgtgagcgtcactacgttctcgttgaatgacacgatacatctccactctac 609
QY 542	TGCTCGGTCGATCGCTGACGACGACGACGACGACGACGACGACGACGACGACG 601
DB 610	tcctcgtcctcactgctgctcctcctcctcctcctcctcctcctcctcctcctc
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Tue May 15 08:41:31 2001

us-09-254-590-21.rng

Page 18

Accession	Sequence	Position
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Db	gctcaacacgggcccctggagaaacagatcgacacgctggcggggaagcttgaatgcctga	1614
Oy	TTTG 1555	
Db	ctcg 1617	

Search completed: May 15, 2001, 01:24:24
Job time: 6485 sec

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GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: May 14, 2001, 23:02:34 ; Search time 2223.07 Seconds
(without alignments)
11543.170 Million cell updates/sec

Title: us-09-254-590-21
Perfect score: 1740
Sequence: 1 ATGACGACGCTGACGAGTACAA.....CTTCATCAGAGAGTACCTAG 1740

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1283235 seqs, 7373929652 residues
Total number of hits satisfying chosen parameters: 2566470

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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10: gb_pat2:**
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB ID	Description
1	1732	99.5	2510	88	AF239613 Homo sapi
2	1495	85.9	1743	95	RU69882 Rattus norv
3	1240.8	71.3	2237	8	AF079372 Gallus ga
4	803.8	46.1	2224	95	RU69884 Rattus norv
5	802.2	46.1	2193	94	AF284345 Rattus norv
6	802.2	46.1	2534	94	AF292389 Rattus norv
7	780	44.8	2521	88	AF031815 Homo sapi
8	776.8	44.6	3095	92	HS4251016 Homo sapi
9	668.4	38.4	2535	93	HSU69883 Rattus norv
10	651.4	37.4	1611	94	RNAF000973 Rattus norv
11	647.6	37.2	1377	95	RU69885 Rattus norv

12	640.2	36.8	2998	94	AF116525	AF116525 Mus muscu
13	529.2	30.4	1956	92	HSAD14	Y08263 H.sapiens m
14	487.2	28.0	114215	70	AC025761	AC025761 Homo sapi
15	487.2	28.0	142190	67	AC021415	AC021415 Homo sapi
16	487.2	28.0	185204	62	AC010595	AC010595 Homo sapi
17	472.6	27.2	164890	66	AC021085	AC021085 Homo sapi
18	425.4	24.4	142190	67	AC021415	AC021415 Homo sapi
19	288.4	16.6	158311	61	AC009589	AC009589 Homo sapi
20	249	14.3	177233	71	AC027645	AC027645 Homo sapi
21	241.8	13.9	1284	9	A95651	A95651 Sequence 1
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23	241.8	13.9	1284	88	AF022150	AF022150 Homo sapi
24	241.8	13.9	1284	92	HSAD000972	HSAD000972 Homo sapi
25	241.8	13.9	2238	9	AX000912	AX000912 Sequence
26	241.8	13.9	2238	88	AF022797	AF022797 Homo sapi
27	241.8	13.9	2261	9	AX000906	AX000906 Sequence
28	240.2	13.8	1982	88	AF033021	AF033021 Homo sapi
29	240	13.8	1278	94	AF072884	AF072884 Mus muscu
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31	240	13.8	1469	94	AF042487	AF042487 Mus muscu
32	239.8	13.8	1278	95	RN0133438	RN0133438 Rattus no
33	238.2	13.7	1278	94	AF149250	AF149250 Rattus no
34	238.2	13.7	1899	94	AF190458	AF190458 Rattus no
35	236.6	13.6	1910	94	AF156554	AF156554 Rattus no
36	216.2	12.4	708	92	HSK00005	HSK00005 Homo sapi
37	216.2	12.4	148822	87	AC020904	AC020904 Homo sapi
38	206.8	11.9	137296	75	AC074162	AC074162 Mus muscu
39	206.8	11.9	184541	75	AC073715	AC073715 Mus muscu
40	206.8	11.9	208113	66	AC019302	AC019302 Mus muscu
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43	156.6	9.0	33520	6	CE02261	CE02261 Caenorhabd
44	135.2	7.8	425	88	AF053403	AF053403 Homo sapi
45	131	7.5	85718	67	AC022660	AC022660 Homo sapi

ALIGNMENTS

RESULT 1
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DEFINITION Homo sapiens apamin-sensitive small-conductance Ca2+-activated
ACCESSION AF239613
VERSION AF239613.1 GI:10334700
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 2510)
AUTHORS Desai, R., Peretz, A., Idelson, H., Lazarovici, P. and Attali, B.
TITLE Ca2+-activated K+ channels in Human Leukemic Jurkat T Cells.
JOURNAL Molecular Cloning, Biochemical and Functional Characterization
J. Biol. Chem. 275 (51), 39954-39963 (2000)
PUBMED 10991935
REFERENCE 2 (bases 1 to 2510)
AUTHORS Desai, R., Peretz, A., Idelson, H., Lazarovici, P. and Attali, B.
TITLE Direct Submission
JOURNAL Submitted (25-FEB-2000) Neurobiology, The Weizmann Institute of
Science, Herzl Street, Rehovot 76100, Israel
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BASE COUNT 639 a 693 c 612 g 566 t
ORIGIN

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Best Local Similarity 99.7%; Pred. No. 0;
Matches 1735; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

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518 CGCGGAGACCTGACGAGATGAGCTAGAGCGGACCGCTGAGCGCGTCCGCTGTC
121 GAGAGAGTGGGCGGCGCTCCCTCCGCTGACGCGCTGCGCGCGCGCTGTTTG
578 GAGAGAGTGGGCGGCGCTCCCTCCGCTGACGCGCTGCGCGCGCGCTGTTTG
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241 CTCATGAGAACCGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG
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760

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us-09-254-590-21.rge

Page 3

[illegible]

Page 4

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 QY 1666 GAGCGGTCCGGTCCGTCGTCGACGAGAGGGGGCGTCTCTTCCACAGACACCAACTTCA 1725
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 Db 1729 TCTAGAGTAGCTAG 1743

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AUTHORS					
TITLE					
JOURNAL					
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AUTHORS					
TITLE					
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FEATURES					
source					
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CDS					
BASE COUNT					

ORIGIN

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 LOCUS RU069884
 DEFINITION Rattus norvegicus calcium-activated potassium channel *ISK* (SK)
 mRNA, complete cds.
 ACCESSION U69884
 VERSION U69884.1 GI:2564071
 KEYWORDS
 SOURCE Norway rat.
 ORGANISM Rattus norvegicus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
 Rattus.
 REFERENCE 1 (bases 1 to 2224)
 Kohler, M., Hirschberg, B., Bond, C.T., Kinzie, J.M., Marillon, N.V.,
 Maylie, J., and Adelman, J.P.
 Small-conductance, calcium-activated potassium channels from
 mammalian brain
 Science 273 (5282), 1709-1714 (1996)
 JOURNAL MEDLINE
 96376602
 REFERENCE 2 (bases 1 to 2224)
 Bond, C.T., Maylie, J., and Adelman, J.P.
 AUTHORS

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 Db 1172 GGTCTGCTGCTTCT 1231
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RESULT 10
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 LOCUS Rattus norvegicus calcium-activated potassium channel (rsk1) mRNA,
 complete cds.

ACCESSION AF000973
 VERSION AF000973.1 GI:2584867
 KEYWORDS
 SOURCE Norway rat.
 ORGANISM Rattus norvegicus
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 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
 Rattus.
 1 (bases 1 to 1611)
 Joiner W.J., Wang, L.Y., Tang, M.D. and Kaczmarek, L.K.
 bsk4, a member of a novel subfamily of calcium-activated potassium
 channels
 Proc. Natl. Acad. Sci. U.S.A. 94 (20), 11013-11018 (1997)
 2 (bases 1 to 1611)
 Joiner W.J., Wang, L.Y., Tang, M.D. and Kaczmarek, L.K.
 bsk4, a member of a novel subfamily of calcium-activated potassium
 channels
 Direct Submission
 Submitted (23-APR-1997) Pharmacology, Yale University, 333 Cedar
 St., New Haven, CT 06520, USA
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 BASE COUNT 331 a 505 c 472 g 303 t
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 Best Local Similarity 69.7%; Pred. No. 2.4e-117;
 Matches 899; Conservative 0; Mismatches 381; Indels 9; Gaps 1;
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 Db 225 CAGGCGAGGCTCAGGGAAGCGCCGACCGGTAGTACACGCCCTGGGCGACCGGTAGGCGCTT 284
 OY 381 GTTCAAGAAAGCGCAAGCGGCTCAGCGACTACGCGCTCATCTTGGCATGTTGGCATCGT 440
 Db 285 CTTCAGAGAGGTAAAGCACTGAGTATGACATCTTTGGCATGTTGGCATGTTGGCATGTT 344
 OY 441 GGTATGTCATGAGACCGAGCTGCTGAGGCGGCTCTGCAAGCAAGCGGTGTAATTC 500
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 OY 501 CTTAGCTCTGAATAGCTTATGAGTCTCTGACAGATCATCTGCTCGGTTGATCATGCT 560
 Db 405 ATTGCGCTGAATAGCTTATGAGTCTCTGACAGATCATCTGCTCGGTTGATCATGCT 464
 OY 561 GTACCGCGCAGGGAATACAGTTGTCATGTCGAGCAATGAGAGAGAGAGAGAGAGAGAG 620
 Db 465 CTACACGCGCCGAGAGATCAGAGCTGTTCTGTCGAGCAATGAGTGCAGATGAGCGGAGAT 524
 OY 621 ACCCATGACTTATGAGCGATTTCTTCACTGCTTGGAAATFACTGCTGTGCTATTTCA 680
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QY	801	TCGTGATTGCCAGAGATCATGCTTTTATCATAGCAAACTTTCACAGTGCCTCCTTAGAG	860
Db	897	CCTGCTGGCTTCGGGTATCTATCCCTGCGACACCGCATCTTCCAGATGCATCCGACG	956
QY	861	CATTGGAGACCTTAATATAGATTAACCTCAATACAGTTTGTATGTAAGACTTTATAGAC	920
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QY	921	TATATGCCCAAGAACTGTACTCTTGGTTTTTAACTATCTCATTTATGATTAATGCCCATG	980
Db	1017	CATCTGCCCCGACACTGTGTTTGGTCTTCAACGCGCTCTCCCTGAGATGGTGGCTG	107
QY	981	GACTGTCCGACTTTGGAAAGGTATACATGATTCAAAGAGATGTACTGTACACTTCTGG	104
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QY	1041	AGCGATGTGGTGTATATCAATTAATCTTTCCTCCATGTGTTATGTCATCTGACTTAA	110
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QY	1101	CACATACGTGTGGAAAGAGAGTGGTCTTACTTACGAAATATGAGTGTCTGTTGGACAGC	118
Db	1197	TACCTTCTGTGGGAAGGTGTGTGTCTGTCTACTGGCATCATGGGAGACAGCTGCATGC	122
QY	1161	CCGTGGTGACTGTAGTGGCAGAGACTTGAACCTTACCAAGCAGAAAAACAGCTGCA	122
Db	1257	ACCTCGTGGGCGCTCTGCTGCTCCGGAAGTTTGGAACTACCAAGCTGAGAACAGCTGCA	133
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QY	1341	AGTAAACAAACATCAAGAAATATCTCGCAAGCTATTTCATAT-----TAAAG	137
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QY	1392	TGTAAAAATGGAACAGAGAACTGTAATGACCAAGCAAACTTTGTGGAGCTTGGCAAA	144
Db	1497	TGTGAAGATTGAACAAAGGAAGGTGAAGCATGACGACACAGCCTGCTGAGCTGGCCAA	157
QY	1452	GACCAGAACATCATGATGATATGTGATTTCTGACTTTAAAGAAAGAGATGAAGACTTGA	157
Db	1557	GGCCACAGAGATTCGATATGATGAGTGGTGTCCAGACTCAGAGCCACAGAGAGGAGTTTGA	167
QY	1512	GAAAGAGATTTGTATCCCTGGGAACAAATAATGAGACTTTGATGGTAGCATCCAGCGCT	157
Db	1617	GGCAGCGCTTATGCCGCTGTGGAGACCGCATGATGATGTCTCTGGTGCCTCCCTGCAAGCTCT	167
QY	1572	CCCTGGGCTCATATACCCAGACCATCAAGC 1600	
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DEFINITION	H.sapiens mRNA for AD14 protein, partial.		PRI
ACCESSION	Y08263		
VERSION	Y08263.1	GI:1770362	
KEYWORDS	AD14 gene.		
SOURCE	human.		
ORGANISM	Homo sapiens		
	Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;		
	Primates; Catarrhini; Hominoide; Homo.		
REFERENCE	I (bases 1 to 1956)		

AUTHORS	Imbert,G., Saudou,F., Yvert,G., Devys,A., Trottier,Y., Garlier,J.M., Weber,C., Mendel,J.L., Cancel,G., Abbaas,N., Duert,A., Didierjean,O., Stevanin,G., Agid,Y., and Brice,A.							
TITLE	Cloning of the gene for spinocerebellar ataxia 2 reveals a locus with high sensitivity to expanded CAG/glutamine repeats							
JOURNAL	Nat. Genet. 14 (3), 285-291 (1996)							
MEDLINE	97051922							
REFERENCE	2 (bases 1 to 1956)							
AUTHORS	Imbert,G.							
TITLE	Direct Submission							
JOURNAL	Submitted (20-SEP-1996) G. Imbert, I.G.B.M.C., Departement of Genetics, B.P. 163, 67404, Illkirch Cedex, FRANCE							
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ORIGIN								
Query Match	30.4%: Score 529, 2; DB 92; Length 1956;							
Best Local Similarity	73.7%: Pred. No. 1.8e-93:							
Matches 687: Conservative	0; Mismatches 243; Indels 2; Gaps 1							
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RESULT	14
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DEFINITION	AC025761 114215 bp DNA HTG 26-SEP-2000 Homo sapiens chromosome 5 clone CTF-109C23, WORKING DRAFT SEQUENCE.
ACCESSION	1 ordered pieces.
VERSION	AC025761
KEYWORDS	AC025761.4 GI:10305165
SOURCE	HTG; HTGS_PHASE2; HTGS_DRAFT. human.
ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
AUTHORS	1 (bases 1 to 114215)
TITLE	DOE Joint Genome Institute.
JOURNAL	Sequencing of Human Chromosome 5 unpublished
REFERENCE	2 (bases 1 to 114215)
AUTHORS	DOE Joint Genome Institute.
TITLE	Direct Submission
JOURNAL	Submitted (14-MAR-2000) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA On Sep 26, 2000 this sequence version replaced gi:7111857.
COMMENT	

```

Web site: http://www.jgi.doe.gov
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Project Information
Center Project Name: 106131
Center clone name: CTR9785RB_109C23
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Summary Statistics
Consensus quality: 112355 bases at least Q40
Consensus quality: 114033 bases at least Q30
Consensus quality: 114204 bases at least Q20
Estimated insert size: 121000; pulse field gel estimation
Estimated insert size: 114265; sum-of-configs estimation
Quality coverage: 6.34 in Q20 bases; pulse field gel estimation
Quality coverage: 6.71 in Q20 bases; sum-of-configs estimation.

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* NOTE: This is a 'working draft' sequence. It currently
* consists of 1 contigs. Gaps between the contigs
* are represented as runs of N. The order of the pieces
* is believed to be correct as given, however the sizes
* of the gaps between them are based on estimates that have
* provided by the submittor.
* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.
  1   114215: contig of 114215 bp in length.
      Location/Qualifiers
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Matches 495; Conservative	0;	Mismatches 13;	Indels 0;	Gaps 0

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AC021415_3	GT7630676
HNG:	HNGS_PHASE1; HNGS_DRAFT.
KEYWORDS	
SOURCE	human
ORGANISM	Homo sapiens
Eukaryota;	Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi,

Tue May 15 08:41:30 2001

us-09-254-590-21.rge

Page 18

Job time: 8326 sec

...

Tue May 15 08:41:29 2001

us-09-254-590-19.tst

OM of: US-09-254-590-19 to: EST: * out_format : pfs

Date: May 14, 2001 9:00 PM

About: Results were produced by the Gencore software, version 4.5,
Copyright (c) 1993-2000 Compugen Ltd.

Command line parameters:

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-MODEL=frame+pn.model -DEV=xlp
-o=/mnt2/1/USPTO.spool/US09254590/runat_14052001.092228.9810/app_query.fasta_1.646
-b=EST -OPMT=fastap -SUFFIX=est -GAPOP=12.000 -GAPEXT=4.000
-MINMATCH=0.050 -XGAPOP=10.000 -XGAPEXT=0.500 -DEL0P=6.000
-GAPEXT=7.000 -XGAPOP=10.000 -XGAPEXT=0.500 -DEL0P=6.000
-FCAPEXT=7.000 -START=1 -MATRIX=blonum62 -TRANS=human40.cdi
-DELETE=7.000 -THR.SCORE=pct -THR.MAX=100 -THR.MIN=0
-LIST=45 -MODE=LOCAL -OUTPMT=pfs -NORM=ext -MINLEN=0
-ALIGN=15 -MODE=LOCAL -USER=US09254590.ecgsl_1.3373 -NCPU=6
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-ICPU=3 -LONGLOG -NO_XLPHY -WAIT -THREADS=1
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Search information block:

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Query: US-09-254-590-19
Query length: 579
Database: EST: *
Database sequences: 9623517
Database length: 73081774
Search time (sec): 1120.600000
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score_list:	strd	orig	zscore	EScore	Len	Documentation
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gb_est77:BE671791	+ 1058.00	1854.38	3.4e-94	689	AA411311 fh1e12.x1 NIH_MGC.17	
gb_est46:AM411311	+ 996.00	1745.54	3.9e-88	635	BE527328 602039710F2 NCI_CGAP.1	
gb_est188:BE527328	+ 978.00	1712.35	5.7e-86	714	BE5297121 601177509F1 NIH_MGC.17	
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gb_est188:AM659534	+ 877.50	1537.13	1.6e-76	562	BR436970 766b05.x1 NCI_CGAP.17	
gb_est187:BF436970	+ 877.50	1532.78	2.8e-76	827	BE306047 601893756F1 NIH_MGC.17	
gb_est185:BF306047	+ 867.00	1519.03	1.6e-75	538	BE20923 202596 MRC 2BOV Bos t	
gb_est18:BE750923	+ 846.00	1481.86	7.5e-71	731	BE51606 Tetradon nigroviridis	
gb_est178:BE751606	+ 823.50	1435.22	1.4e-70	985	AL277340 Tetradon nigroviridis	
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gb_est16:BG115017 - 465.00 799.76 1.9e-35 1057 | BG115017 602315701F1 NIH_MGC
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seq_documentation block: 754 bp mRNA EST 08-SEP-2000
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DEFINITION 7445610.x1 NCI_CGAP.P70604 CALCIUM-ACTIVATED POTASSIUM CHANNEL
similar to TR.P70604 P70604 CALCIUM-ACTIVATED POTASSIUM CHANNEL
RSK2.1; mRNA sequence.

ACCESSION BE671791.1 GI:10032332
VERSION BE671791.1
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 754)
NCI_CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert.Strausberg@nih.gov

COMMENT Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael
R. Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
Bonaldo, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
CDNA Sequencing by: Washington University Genome Sequencing Center
DNA Sequencing by: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL, send email to:
infoimage.llnl.gov
Seq primer: -400P from Glibco
High quality sequence step: 482.

Location/Qualifiers
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="NCI_CGAP.GC6"
/note="Vector: pT73D-Pac (Pharmacia) with a modified
polylinker. Plasmid DNA from the normalized library
in polylinker. Plasmid DNA was prepared, and ss circles were made in
vitro. Following HAP purification, this DNA was used as
tracer in a subtractive hybridization reaction. The driver
was PCR-amplified cDNAs from a pool of 5,000 clones made
from the same library (clones 1257096-1258631,
146064-1470983, and 1475592-1476743). Subtraction by
Bento Soares and M. Fatima Bonaldo.

BASE COUNT 157 a 232 c 213 g 151 t
ORIGIN
alignment_scores: Length: 251
Quality: 1253.00 Gaps: 0
Ratio: 5.073
Percent Similarity: 98.406 Percent Identity: 97.610

Alignment block:
US-09-254-590-19 x BE671791 ..
Align seg 1/1 to: BE671791 from: 1 to: 754

12 ArgProLeuSerAsnLeuSerAlaSerArgArgAsnLeuHisGluMetas 28
|||||
2 CGGCGCGTCAGCACTTGACGCGTCGCGCGGACCTGACGCGAGGAG 51

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28 pSerGluAlaGlnProLeuGlnProPheAlaSerValGlyGlyGlyG 45
|||||
52 CTCAGAGCGCCAGCCCTCTGACAGCCCGGGCTGTGCGAGAGAGTGGC 101
|||||
45 1yAlaSerSerProSerAlaAlaAlaAlaAlaAlaAlaAlaValSerSer 61
|||||
102 GCGGCTCTCCCGCTGTGACAGCCCGCGCCCGCGCGCTTTGCTCC 151
|||||
62 SerAlaProGluIleValValSerLysProGluHisAsnAsnSerAsnAs 78
|||||
152 TCAGCCCCCGAGATCGTGTCTCAAGCCCGAGCACAACATCCACACAA 201
|||||
78 nLeuAlaLeuTyrGlyThrGlyGlyGlyGlyGlyGlyGlyGlyGlyG 95
202 CCGGCGCTCTATGGAACCGCGCGGAGGAGGAGGAGGAGGAGGAGG 251
95 1yGlyGlyGlySerGlyHisGlySerSerSerGlyThrLysSerSerLys 111
252 GCGGTGGCGGAGCGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 301
|||||
112 LysLysAsnGlnAsnIleGlyTyrLysLeuGlyHisArgAlaAlaLeu 128
|||||
302 AAGAAAAACCAAGAACATCGGTACACAGCTGGCCACCGCGCGCTGTT 351
|||||
128 eGluLysArgLysArgLysSerSerSerSerSerSerSerSerSerSer 145
352 CGAAAAAGCGCAAGCGCTCAGCGAGCTACGCGCTCATCTTCGCGATG 401
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145 1yIleValValMetValIleGluThrGluLeuSerTyrGlyAlaTyrAsp 161
402 GCATCGCTGCTCATGCTCATGTCGAGACGAGCTGCTGGGCGCTTCAGC 451
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162 LysAlaSerLeuTyrSerLeuAlaLeuLysCysLeuLysLeuSerTh 178
452 AAGGCGCTGCTGTATCTCTAGCTGGAATGCTTCATGCTCTCCAC 501
178 rIleIleLeuLeuGlyLeuIleLeuValTyrHisAlaArgGluIleGln 195
502 GATCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 551
195 eUpHemeValAspAsnGlyAlaAspAspTyrArgIleAlaMetThrTyr 211
552 TGTTCATGCTGCAAAATGAGCAGATGACAGCTGAGATACCTGACTTAT 601
212 GUAArgLysPhePheIleCysLeuGluIleValCysAlaIleHisPr 228
602 GAGCGTATTTTCTTCATCTGCTGGAATATGCTGTGCTATTCATCC 651
228 oLleProGlyAsnTyrThrPheThrPheThrAlaArgLeuAlaPheSer 245
652 CATACCATGCGCATTTATCATTCACATGAGCTGCCCGCTGCTCTCT 701
245 1yAlaProSerThrThrAlaAspValAspIleIleLeuSerLeuPro 261
702 ATGCCCATCCACACACCGCTGATGATAGTACTGATATCTATACCA 751
262 Met 262
752 Arg 754

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seq_name: gb_est46:AW411311

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 DEFINITION fhl1e12.x1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2964598 5',
 mRNA sequence.
 ACCESSION AW411311
 VERSION AW411311.1 GI:693852
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Cephalata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
 1 (bases 1 to 689)
 NIH-MGC http://mgi.nci.nih.gov/
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 CONTACT Robert Strausberg, Ph.D.
 COMMENT Tel: (301) 496-1550
 Email: Robert.Strausberg@nih.gov
 Tissue Procurement: ATCC
 CDNA Library Preparation: Ling Hong/Rubin Laboratory
 DNA Sequencing by: The I.M.A.G.E. Consortium (LMU)
 Sequencing Center (NISC)
 Clone Distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 www.bio.llnl.gov/dbp/image/image.html
 Plate: LCM64 row: J column: 23
 Seq primer: -21M13 forward primer (ABI).
 Location/Qualifiers
 1..689
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:2964598"
 /clone_lib="NIH_MGC_17"
 /tissue_type="rhodomyosarcoma"
 /lab_host="DH10B (phage-resistant)"
 /note="Organ: muscle; Vector: pORS7; Site_1: EcoRI;
 Site_2: XhoI; cDNA made by oligo-dT priming.
 Directionally cloned into EcoRI/XhoI sites using the
 following 5' adaptor: GGCACGAG(G). Size-selected
 for average insert size 1.8kb. Library constructed by
 Ling Hong in the laboratory of Gerald M. Rubin (University
 of California, Berkeley) using ZAP-CDNA synthesis kit
 (Stratagene) and Superscript II RT (Life Technologies)."
 BASE COUNT 132 a 167 g 178 t
 ORIGIN

alignment_scores:
 Quality: 1058.00
 Ratio: 4.831
 Percent Similarity: 96.903
 Percent Identity: 89.823

alignment_block:
 US-09-254-590-19 x AW411311 ..
 Align seg 1/1 to: AW411311 from: 1 to: 689

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160 rAspLysAlaSerLeuTyrSerLeuAlaLeuLysCysLeuLysLeuSer 177
|||||
61 CTCGAAGGACCTCATGTTTTCGTTGCTGAGCTGAAATGCTTATCATCTGT 110
177 eThrIleIleLeuGlyLeuIleValTyrHisAlaArgGluIle 193
|||||
111 CCACCATCATCTTTGGCTTGATCATCGCTACACACACACACACACACAC 160
194 GlnLeuPheMetValAspAsnGlyAlaAspAspTyrArgIleAlaMet 210
161 GAGCTCTTCTGATTCGACACACGCGGAGATGATGCGGATGATGATGAT 210
210 rTyrGluArgIlePhePheIleCysLeuGluIleValCysAlaIleHis 227
211 CTACGACGCGATCTCATCATCAGCCCTGGATGCTGTGCGCCATCC 260
227 1sProIleProGlyAsnTyrThrPheThrThrAlaArgLeuAlaPhe 243
261 ACCCATCTCTGCGAGTCAAGTCTTCTGAGCGGACGCTGCGCTTC 310
244 SerTyrAlaProSerThrThrAlaAspValAspIleLeuSerTyr 260
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Tue May 15 08:41:29 2001

us-09-254-590-19.rst

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311 TCCTACACACCTCCCGGCGAGCCGATGAGACATCATCTCTCTAT 360
260 EPrometheuAArgLeuTyrLeuIleAlaArgValMetLeuLeuHis 277
|||||
361 CCCCATGTTCTCGGCTGCTACTGATGCGCCGAGTCAATGCTGTCGACA 410
277 erLysLeuPheThrAspAlaSerSerArgSerIleGlyAlaLeuAnlys 293
|||||
411 GCAAGCTCTCACCAGATGCTCCTCCGACATCGGGGCGCTCAACAG 460
294 IleAspPheAsnThrArgPheValMetLysThrLeuMetThrIleCysP 310
461 ATCACTTCACACCCGCTTGTGATGAGAGCGCTCATGACATCTGCCC 510
310 oglyThrValLeuLeuValPheSerIleSerIlePheIleAlaIle 327
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511 TGGCAGTGTCTGCTGCTGTCAGCATCTCTGATCATCTGCTGCT 560
327 rPlhrValArgAlaCysGluArgTyrHisAspGlnGlnAspValThrSer 343
|||||
561 GGACGCTGCTGCTGCTGTAAGAGTACATGACACAGACAGTACTAGT 610
344 AsnPheLeuGlyAlaMetThrLeuIleSerIleThrPheLeuSerIleG 360
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611 AACTTCTGGTGGTCCATGTCATCTCCATCATCATCTTCTTCATTGG 660
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DEFINITION 5', mRNA sequence.
ACCESSION BF527328.1 GI:11614691
VERSION BF527328.1
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eultheria; Primates; Catarrhini; Hominoidea; Homo.
REFERENCE 1 (bases 1 to 635)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/
TITLES National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert.Strausberg@nih.gov
Tissue procurement: David N. Louis, M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Jockey Genomics, Inc.
DNA distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov
plate: L1AM9484 row: C column: 04
High quality sequence stop: 631.
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FEATURES

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loss"
/lab_host="DH10B (TI phage-resistant)"
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Site_2: Salt; Cloned: unidirectionally; Primer: Oligo dt.
Average insert size 2.3 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP library."
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BASE COUNT

156 a 155 c 139 g 185 t

ORIGIN

alignment_scores: 996.00 Length: 212
Quality: 4.743 Gaps: 2
Percent similarity: 99.057 Percent identity: 99.057

alignment_block:
us-09-254-590-19 x BF527328

Align seq 1/1 to: BF527328 from: 1 to: 635

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1 GAAAGCGGAGCGGCTCAGCGACTACGAGCTGCTGCTGCTGCTGCTGCTG 50
145 ylleValValMetValIleGluThrGluLeuSerTyrGlyAlaTyrAsp 162
51 CATGCTGCTCATGCTCATGCTCATGCTCATGCTCATGCTCATGCTCATG 100
162 ysaLaserLeuTyrSerLeuAlaLeuLysCysLeuIleSerLeuSerThr 178
101 AGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 150
179 llelleLeuLeuGlyLeuIlelleValTyrHisAlaArgGluIleGln 195
151 ATCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 199
195 urPheMetValAspAsnGlyAlaAspAspTyrArgIleAlaMetThrTyr 212
200 GTTTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 249
212 llaArgIlePhePheIleCysLeuGluIleLeuValCysAlaIleHisPro 228
250 AGCGATATTTCTCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 239
229 llaProGlyAsnTyrThrPheThrTyrPheAlaArgLeuAlaPheSerTy 245
300 ATTCCTGGGATATATACATTCACATGAGGCGGCGCTGCTGCTGCTGCT 349
245 ralaProSerThrThrAlaAspValAspIlelleLeuSerIleProm 262
350 TGCCCCATCCACACACACCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 399
262 etPheLeuArgLeuTyrIleuIleAlaArgValMetLeuLeuHisSerLys 278
400 TGTCTTACACCTCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 449
279 leuPheThrAspAlaSerSerArgSerIleGlyAlaLeuAnlysIleAs 295
450 CTTTCACTGATGCTCCTCTAGAGCAATGGAGCACTTAATAGATPAA 499
295 nPheAsnThrArgPheValMetLysThrLeuMetThrIleCysProGlyT 312
500 CTTCATACACGCTTCTGCTATGACACTTAAAGACTATATGCCAGGAA 549
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DEFINITION mRNA sequence.
ACCESSION BE297121 GI:9180693
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Tue May 15 08:41:29 2001

us-09-254-590-19.1st

Page 4

KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
REFERENCE Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS 1 (bases 1 to 714)
TITLE NIH-MGC http://mgi.nci.nih.gov/
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert.Strausberg@nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Ling Hong/Rubin Laboratory
DNA Sequencing by: The I.M.A.G.E. Consortium (LNL)
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at: image.lnl.gov
Plate: LNC209 row: a column: 04
High quality sequence stop: 613.

FEATURES
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Location/Qualifiers
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/db_xref="taxon:9606"
/clone="IMAGE:3532683"
/issue_type="NIH-MGC_17"
/lab_host="Phadomyosarcoma"
/note="Organ: muscle; Vector: pOTB; Site: 1: EcoRI;
Site: 2: XhoI; CDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCACGAG(G). Size-selected >500bp
ling Hong in the laboratory of Gerald M. Rubin (University
of California, Berkeley) using ZAP-CDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."

BASE COUNT 126 a 226 c 178 g 184 t
ORIGIN

alignment_scores:
Quality: 978.00
Ratio: 4.425
Percent Similarity: 93.249
Percent Identity: 83.966
Alignment_block:
US-09-254-590-19 x BE297121 ..
Align seg 1/1 to: BE297121 from: 1 to: 714

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|||||
1 GTGATAGAGCCGACCTCTCTGGGTTTGTACTCAAGACCTCATGTT 50
166 rSerleuAlaLeuLysCysLeuLeuSerLeuSerThrlleLeuLeuG 183
|||||
51 TTGCTTGGCCCTGAATGCTTATCTGCTGTCACCATCATCTTTGG 100
183 lyeuIlelleValTyrlsAlaArgluileGluLeuPheMetValasp 199
|||||
101 GCTGATCATCGCTACACACCTGAGTCCAGCTTCCTGATTCGAC 150
200 AsnglyAlaAspAPrrPARgllleAlaMetThrTyrgluArgllePhep 216
151 AACGGCGGATGACCTGGGATGATGATGATGATGATGATGATGATG 200
216 eliecyLeuGluileLeuValCyAlaIleHsProlleProGlyasnT 233
201 CATGACCTGAGATGCTGTGTGCGCATCCACCATCTCTGCGAGT 250
233 yrrhPheThrTPThrlaArgleuAlaPheSerTyraLaseLeuThr 249
251 ACAAGTTCCTTGAGAGCGACGCTGCTCTCTCATACACCTCCCGG 300

250 ThrThraAlaSPyAlaSPlelleLeuSerllePromeThreLeuArgle 266
301 CGGAGGCGCCATGTGACATCATCTGTCTATCCCAATGTTCTGGCGCT 350
266 uTyrllelleAlaArgValMetleuLeuHsSerLysLeuPheThraspa 283
351 GTACACGATGCGCCGATGATGATGATGATGATGATGATGATGATG 400
283 laseSerArgSerlleGlyAlaLeuAsnLysIleAsnPhelaSnhrarg 299
401 CTTGCTGCGGACGATGCGGCGCCCTCAACAGATCACTTCAACCGCC 450
300 PheValMetLysThrlleuMetThrllecyProGlyThValleuLeu 316
451 TTTGTCATGAGAGCGCTCATGACATGACATGACATGACATGACAT 500
316 lPheSerlleSerleuThrllelleAlaAlaTPThraValArglaCysg 333
501 GTTCAGATCTCTCTGTGATCATGCTGCTGCTGCTGCTGCTGCTG 550
333 lUArgTyrlsAspGlnGlnAspValThrSerAsnPhelaGlyAlaMet 349
551 AAAGTACATGACACGACGACGCTACTAGTACTTCTGAGGACATG 599
350 TrpleuileSerlleThrlleuSerlleGlyTyrglyaspMetValpr 366
600 TGGCTATCTCATCATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 649
366 oAnFrThrTyrcysGlysglyValCysleuLeuThrglyleMetGly 382
650 C...CATACCTGTGGAG...GTGCTCTCTCTCAACGCTGAGGCT 693
383 AlaglyCys 385
694 GCGGCTGT 702

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seq_documentation_block:
LOCUS AM659534 521 bp mRNA
DEFINITION 96789 MARC IBOV Bos taurus CDNA 5', mRNA sequence.
ACCESSION AM659534
VERSION AM659534.1 GI:7425361
KEYWORDS EST.
SOURCE
ORGANISM Bos taurus

REFERENCE
AUTHORS
1 (bases 1 to 521)
Smith, T.P.L., Casas, E., Stone, R.T., Heaton, M.P., Grosse, W.M.,
Bennett, G.A., Fahrenkrug, S.C., Fieking, B.A., Rohrer, G.A., Laegreid
Design and use of four pooled tissue normalized cDNA libraries for
EST discovery in cattle
Unpublished (2000)
Contact: Smith TP
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Email: smithemall@marc.usda.gov

TITLE
JOURNAL
COMMENT
Single pass sequencing. Bases called and alt-trimmed with phred
v0.980904.e. Vector identified by cross-match with the -minscore 18
PCR primers
FORWARD: AGGAACACTATGACAT
BACKWARD: GTTTCCTGACGACGACG
Plate: 74 row: J column: 10
Seq primer: ATTAGGTGACACTATGAG
Location/Qualifiers
1..521

FEATURES
Source
Location/Qualifiers
1..521

81 utyrclgthrcgylgylgylserthrgylgylgylgylgylg 98
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 204 CTATGTAACCGCGCGGAGGACGACGAGGAGGCGGCGGCG 253
 98 1ySerg1yH1s1ySerg1yH1ySerg1yH1ySerg1yH1y 114
 |||
 254 GGAGCGGCGGACGAGGAGGAGGAGGAGGAGGAGGAGGAG 303
 115 G1nAen11eG1y1y1y1y1y1y1y1y1y1y1y1y1y1y 131
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 304 CAGAACATCGGCTACAGCTGAGGCGGCGGCGGCGGCGG 353
 131 g1ySAr1g1eUSeAr1p1y1y1y1y1y1y1y1y1y1y 148
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 354 CAAGCGGCTCAGCGACTACCGCTCTTCGCGATGTCGCG 403
 148 a1Me1yA11eG1y1y1y1y1y1y1y1y1y1y1y1y1y 164
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 404 TCATGGTCATCAGACGACGACTGCTGCGGCGGCTCAG 453
 165 Leu1ySer1eUa1eU1y1y1y1y1y1y1y1y1y1y1 181
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 454 CTGTATTCCTAGCTTGAATGCCCTATCAGCTCTCCAG 503
 181 u1eUa1y1eU1e1y1y1y1y1y1y1y1y1y1y1y1y 198
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 504 GCTCGGCTGATCATCTGTACACGCGGAGAAATACCT 553
 198 a1Asp 199
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 554 AGGAT 558

seq_name: gb_est85:BF306047

seq_documentation_block: 827 bp mRNA EST 21-NOV-2000
 LOCUS BF306047
 DEFINITION 601893756f1 NIH-MGC_17 Homo sapiens CDNA clone IMAGE:4139388 5',
 mRNA sequence.
 ACCESSION BF306047
 VERSION BF306047.1 GI:11253116
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 827)
 AUTHORS NIH-MGC http://mgc.ncl.nih.gov/
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Tel: (301) 496-1550
 Email: Robert.Strausberg@nih.gov
 Tissue Procurement: ATCC
 CDNA Library Preparation: Ling Hong/Rubin Laboratory
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
 Plate: L1CM1049 row: P column: 13
 High quality sequence stop: 731.
 Location/Qualifiers
 1..827
 /organism="Homo sapiens"
 /db_xref="taxon:3606"
 /clone="IMAGE:4139388"
 /clone_lib="NIH-MGC_17"
 /tissue_type="pharyngosarcoma"
 /lab_host="DH10B (phage-resistant)"
 /note="Organ: muscle; Vector: pOT87; Site: 1: EcoRI;
 Site: 2: XhoI; CDNA made by oligo-dT priming.
 Directionally cloned into EcoRI/XhoI sites using the
 following 5' adaptor: GGCAACGAG(G). Size-selected >500bp

for average insert size 1.8kb. Library constructed by
 Ling Hong in the Laboratory of Gerald M. Rubin (University
 of California, Berkeley) using ZAP-cDNA synthesis kit
 (Stratagene) and Superscript II RT (Life Technologies)."

BASE COUNT 159 a 247 c 223 g 198 t
 ORIGIN

alignment_scores:
 Quality: 877.50 Length: 233
 Ratio: 4.007 Gaps: 3
 Percent Similarity: 93.991 Percent Identity: 85.408

alignment_block:
 US-09-254-590-19 x BF306047 ..
 Align seg 1/1 to: BF306047 from: 1 to: 827

168 Leu1a1eU1y1y1y1y1y1y1y1y1y1y1y1y1y1y 184
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 134 GTGGCCCTGAAATCCCTTATCAGTCTGCCACATCATCTT 182
 184 u1e1y1y1y1y1y1y1y1y1y1y1y1y1y1y1y1y1y 201
 |||
 183 GATCATCGCTACACACACAGCTGAAAGCTTCGATCGAC 222
 201 1y1a1a1p1y1y1y1y1y1y1y1y1y1y1y1y1y1y 217
 |||
 233 GCGCGGATGACTGGCGGATGACCTGACGAGCGATCTT 282
 218 Cys1eUg1u1eUa1y1y1y1y1y1y1y1y1y1y1y1y 234
 |||
 283 AGCTTGAGAGTCTGCTGCTGCGGACATCCACCCATTC 332
 234 rPhet1y1y1y1y1y1y1y1y1y1y1y1y1y1y1y1y 251
 |||
 333 GTTCTCTGAGCGGACGCGCTGCTCTCTACACACCTCC 382
 251 h1y1a1y1a1p1y1y1y1y1y1y1y1y1y1y1y1y1y 267
 |||
 383 AGGCCATGTGACATCATCTGTATCCCATGCTCCGCG 432
 268 Leu1e1a1a1y1y1y1y1y1y1y1y1y1y1y1y1y1y 284
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 433 CTATGCGCGGAGTATGCTGCTGACAGCAAGCTTCC 482
 284 rSer1ySer1e1y1y1y1y1y1y1y1y1y1y1y1y1y 301
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 483 GTCCGCGACATCGGCGGCTCAACAAATCACTCAACCC 531
 301 a1Me1y1y1y1y1y1y1y1y1y1y1y1y1y1y1y1y1y 317
 |||
 532 TCATGAGAGCTCATGACATCTGCTTGGACTGCTGCT 580
 317 Ser1ySer1e1y1y1y1y1y1y1y1y1y1y1y1y1y 334
 |||
 581 AGCATCTCTCTGATCATCTTGGCTGACCTGCTCTG 630
 334 g1y1y1y1y1y1y1y1y1y1y1y1y1y1y1y1y1y 350
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 631 GTACCATGAGCAGCAGGAGCTAAGTAACTTTCGCTG 680
 351 Leu1e1y1y1y1y1y1y1y1y1y1y1y1y1y1y1y1y 367
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 681 TCATCATCATCATCTTCCATCTGTTATGGGAGCATG 729
 367 n1y1y1y1y1y1y1y1y1y1y1y1y1y1y1y1y1y 384
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 730 CACATCATGAGGAGGAGGAGGAGGAGGAGGAGGAGG 778
 384 1yCys1y1y1y1y1y1y1y1y1y1y1y1y1y1y1y1y 398
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 779 GTTCATGAGCGCTGTGCTGCGGCGG...GCCCAAGTGGAT 820

Library made from pooled tissue from testis, thymus, semitendinosus muscle, longissimus muscle, pancreas, adrenal, and endometrium."

BASE COUNT 185 a 118 c 134 g 101 t

ORIGIN

alignment_scores:
Quality: 846.00 Length: 179
Ratio: 4.862 Gaps: 0
Percent Similarity: 97.207 Percent Identity: 94.413

alignment_block:
US-09-254-590-19 x BE751606 ..

Align seg 1/1 to: BE751606 from: 1 to: 538

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383 AlAGLCysThrAlaLeuValAlaValAlaAlaArgLysLeuGluLe 399
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1 GCGGTTCACACGCCCTGGGGAGCTGTGTAGCAAGAACTGAACT 50
|||||
399 uThrlYsAlaGluLysValHisAsnPhenMetCaspThrGlnLeuT 416
|||||
51 TACCAAGACGAGAAAGCACCTGCACACTCATGATGACACTGACGCTGA 100
|||||
416 hTrLysArgValLysAsnAlaAlaAsnValLeuArgGluThrLysLeu 432
|||||
101 CAAAAAGAGTGAATAATGCCGCTGCCATGTACTCGAGGAACATGGCTA 150
|||||
433 IleTyrLysAsnThrLysLeuValLysLysIleAspHisAlaLysValAr 449
|||||
151 ATTTCAGAAATATACAAAGCTAGGAAAAAGTAGATCATGCAAAAGCTAG 200
|||||
449 gLysHisGlnArgLysPheLeuGlnAlaIleHisGlnLeuArgSerValL 466
|||||
201 AAACATCAACGCGAAATCTTGCACAGCATTCATCAATTGAGAGAGTGA 250
|||||
466 yMetGluGlnArgLysLeuAsnAspGlnAlaAsnThrLeuValAspLeu 482
|||||
251 AAATGACACAGAGAGAGCTGAACGACGCAACCTGGTGGAGCTG 300
|||||
483 AlaLysThrGlnAsnIleMetLysAspMetLysSerAspLeuAsnGluAr 499
|||||
301 GCGAAGACTCAGAACATCATGATGACATGATTCGCACTTAATGAAAG 350
|||||
499 gSerGluAspPheGluLysArgGlyLeuValThrLeuGluThrLysLeuG 516
|||||
351 AAGTGAGACTTTGAGAGAGAGATCGTTACCTGGAACGAAGTTAGAGA 400
|||||
516 hTrLeuIleGlySerIleHisAlaLeuProGlyLeuIleSerGlnThrIle 532
|||||
401 CTTTGATGTTGATGATCATCATCCCTGCTGGCTCATTAAGCAACACATC 450
|||||
533 ArgGlnGlnArgAspPheIleGlnAlaGlnMetGluSerTyrLysArg 549
|||||
451 AGGAGAGAGAGAGAGACTTCTCTGAGAGCTCGATGAGACAACTAGCGCA 500
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549 sHisValThrTyrAsnAlaGluArgSerArgSerSer 561
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501 GCACATTCCTCTAGACGCTGAAAGCTCGCGTCTCG 537

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seq_name: gb_gss31:CNS0462N

seq_documentation_block:

LOCUS CNS0462N 985 bp DNA GSS 18-MAY-2000

DEFINITION Tetradon nigroviridis genome survey sequence PUC-ori end of clone 086H23 of library G from Tetradon nigroviridis, genomic survey sequence.

ACCESSION AL277340

VERSION AL277340.1 GI:8011543

KEYWORDS GSS: genome survey sequence.

SOURCE Tetradon nigroviridis.

ORGANISM Tetradon nigroviridis

REFERENCE
AUTHORS
TITLE
JOURNAL
REFERENCE
AUTHORS

TITLE
JOURNAL
REFERENCE
AUTHORS
JOURNAL
REFERENCE
AUTHORS
COMMENT
FEATURES
SOURCE

location/Qualifiers

1..985
/organism="Tetradon nigroviridis"
/db_xref="taxon:99883"
/clone="086H23"
/clone_lib="G"
/note="Genoscope sequence ID : C086086CD12SP1-end : PUC-ori"

BASE COUNT 223 a 244 c 256 g 260 t 2 others

alignment_scores:
Quality: 823.50 Length: 298
Ratio: 3.866 Gaps: 4
Percent Similarity: 71.477 Percent Identity: 57.047

alignment_block:
US-09-254-590-19 x CNS0462N ..

Align seg 1/1 to: CNS0462N from: 1 to: 985

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45 GCGCAAGACAGAGAGAGAGATCGGCTGCGGCTGCGGACAGAGA 94
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125 gAlaLeuPheGluLysArgLysArgSerAspLysPheAlaLeuIlePheG 142
|||||
95 GCGCTCTTTGGGAGAGCGCAAACTGTTGAGCATTTACCGCTGTGTG 144
|||||
142 LysMetPheGlyLysValMetValIleGluThrGlnLeuSerTyrGly 158
|||||
145 GCATGTTTGGATTTTGTGATGTGTGTGTTGAGAGAGAGCTGTGAGAGGC 194
|||||
159 AlaTyrAspLys..... 162
|||||
195 ATTATATAGCAAGGTGAGTCTCTGTGATTTATCAATTAATCTTTAGC 244
|||||
162 ..... 162
|||||
245 TTCCTGATTAACATCTGTGATGACATATACATAGGTGTTCTCAATGC 294
|||||
163 .....Ala.SerLeuTyrSerLeuAlaLeuLysCy 172
|||||
295 TGTGTCTTCATTTTCTCTAGGAATCGTATATTTCACAGCTGTAAAGGG 344

```


172 sleuileuSerleuSerThrIleleuLeuGlyleuIleleuValTyrH 189
 345 CCTGATCAGTGTTCACGGCTGTGTTGGTCTCAATATGTATGAC 394
 189 lsAlaAAGlu..... 192
 395 ATGCACGGGAATTCAGCAGCTGGACAAAGGACCAAGAAATCTGAT 444
 192 192
 445 TTAGATATGAGACCAACACTTCCTCGAATGATCAGTGAAGTTCT 494
 193 193
 495 TCTTCCTTTCTTCTGAGCTGTTCAGTGTGACAAACGTCGACAGCTGG 544
 206 ArgIleAlaMetThrTyrGluArgIlePhePheIleCysLeuGluIle 222
 545 AGGATAGCTATGACCTTGTGACGGATTTCTTTGTCTGTCTGAGCTCT 594
 222 uValCysAlaIleHisProIleProGlyAsnTyrThrPheThrTyr 239
 595 CGTCTGCTCCATCCATCCGTCGACGACCAATACGTTCTCAGCTGACCA 644
 239 laArgLeuAlaPheSerTyrAlaProSerThrThrAlaAspValAsp 255
 645 CCGCTCTGCGCCGACGCTACACCGCGCGCGCTGACGCTGAGAC 694
 256 IleIleLeuSerIleProMetPheLeuArgLeuTyrIleuIleAlaArg 272
 695 GTCTATCTTTCTGTGCGGATGTCCTGCGCTCTTACCTGATGCGGGGT 744
 272 MetLeuLeuHisSerIleuPheThrAspAlaSerSerArgSerIleG 289
 745 GATGCTGCTCCACAGAACTCTTACGACGCTTCTCCCGGAGATCG 794
 289 lAlaLeuAsnLysIleAsnPheAsnThrArgPheValMetLysThrIleu 305
 795 GGGCCTCAACAAGATCAGCTTGTACACTGCTTCGTGATGAAAGACGCTG 844
 306 MetThrIleCysProGlyThrValleuLeuValPheSerIleSerIleu 322
 845 ATGACATCTGCCCTGTAAGCTGCTGCTGCTGCTGCTGCTGCTGCTG 894
 322 PileIleAlaIleThrThrValArgAlaCysGluArgTyr 335
 895 GAKCATGCTGCGTGAAGCTGTGCTGTCTGTGATGAGATAT 934
 seq_name: gb_est73:BE397619
 seq documentation_block: 731 bp mRNA EST 21-JUL-2000
 LOCUS BE397619 601289492P1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3620014 5',
 DEFINITION mRNA sequence.
 ACCESSION BE397619
 VERSION BE397619.1 GI:9342984
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 731)
 AUTHORS NIH-MGC http://mgi.nci.nih.gov/.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Tel: (301) 496-1550
 Email: Robert.Strausberg@nih.gov
 Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
 CDNA Library Preparation: Ling Hong/Rubin Laboratory
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
 Plate: LUCM291 row: 9 column: 23
 High quality sequence start: 3
 High quality sequence stop: 662.
 Location/Qualifiers

FEATURES

1. 731
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:3620014"
 /clone_1ib="NIH_MGC_8"
 /clone_type="purified lymphoma"
 /lab_host="DH10B (phage resistant)"
 /note="Organ: lymph. Vector: pORF7. Site 1: XhoI; Site 2:
 EcoRI; cDNA made by oligo-dT priming. Directionally
 cloned into EcoRI/XhoI sites using the following 5'
 adaptor: GGCACGAG(5). Size-selected >500bp for average
 insert size 1.8kb. Library constructed by Ling Hong in
 the laboratory of Gerald M. Rubin (University of
 California, Berkeley) using ZAP-cDNA synthesis kit
 (Stratagene) and Superscript II RT (Life Technologies)."
 BASE COUNT 142 a 220 c 187 g 182 t
 ORIGIN

alignment_scores:
 Quality: 819.00 Length: 205
 Ratio: 4.356 Gaps: 4
 Percent Similarity: 91.707 Percent Identity: 81.463

alignment_block:
 US-09-254-590-19 x BE397619 ..

Align seg 1/1 to: BE397619 from: 1 to: 731

143 MetPheGlyIleValIleMetValIleGluThrGluLeuSerTyrGlyAl 159
 127 TTTGTTGGTGTTCCTTCAAGTTATAGAT.....GGAGA 161
 159 aTyrAspLysAla..SerLeuTyrSerLeuAlaLeuLysCysLeuIleSer 175
 162 GACCTATTAAGGACTCTTTGTTGTTGGCTGCTGCAAAATCCCTATAGT 211
 176 LeuSerThrIleIleLeuLeuGlyLeuIleIleValTyrHisAlaArg 192
 212 CTGTCCACCATCATCTTTGGCTGATCATCCCTACACACAGCTGA 261
 192 uIleGluLeuPheMetValAspAsnGlyAlaAspAspTyrArgIleAla 209
 262 AGTCCAGCTCTTGTGATGACAAATGCGCGGATGATGCGGATAGCCA 311
 209 eThrTyrGluArgIlePhePheIleCysLeuGluIleLeuValCysAla 225
 312 TGACCTACGAGCGCATCCTGTACATCAGCTCGAGATCTGTGTGCGCC 361
 226 IleHisProIleProGlyAsnTyrThrPheThrTyrThrAlaArgLeuAl 242
 362 ATCCACCCCATTCCTGCGAGTACAAAGTCTTCTGAGCGAGCGCTGGC 411
 242 aPheSerTyrAlaProSerThrThrThrAlaAspValAspIleIleLeu 259
 412 CTTCCTCTACACACCTCCCGCGGAGCGCGGATGTGACATCATCTCTGT 461
 259 eTlePrometPheLeuArgLeuTyrIleuIleAlaArgValMetLeuLeu 275
 462 CTAATCCCATGTTCTGCGCTGTAATCCTGATCCCGGATCATCTCTCTG 511
 276 HisSerLysLeuPheThrAspAlaSerSerArgSerIleGlyAlaLeuAs 292
 512 CACACCAAGCTCTTACCATGCTCTGCTCCGCGAGATGGGCGCCCTCA 561
 292 nLysIleAsnPheAsnThrArgPheValMetLysThrLeuMetThrIleC 309
 562 CAAGATCAACTTCAACACCGCTTGTGATGAGAGAGCTCATGACATCT 611

Tissue Procurement: Michael J. Brownstein, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D.

CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/URL at:
www.bio.lnln.gov/dbip/image/image.html

Seq primer: -40UP from Gibco
High quality sequence stop: 456.

FEATURES

Source Location/Qualifiers
1. 475
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2248309"
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/sex="male"
/dev_stage="adult"
/lab_host="DH10B"
/note="Organ: prostate; Vector: pT73D-Pac (Pharmacia) with a modified polylinker; Plasmid DNA from the normalized library NCI-CGAP_P128 was prepared, and ss circles were used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (clonoids 985608-986759, 1101192-1101959, and 1217928-1220615)."
Subtraction by Bento Soares and M. Fatima Bonaldo.
BASE COUNT 92 a 161 c 148 g 73 t 1 others
ORIGIN

alignment_scores:
Quality: 781.50 Length: 158
Ratio: 5.010 Gaps: 1
Percent Similarity: 98.734 Percent Identity: 98.101

alignment_block:

US-09-254-590-19 x A1810558 ..

Align seg 1/1 to: A1810558 from: 1 to: 475

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2  CGCGGAGACCTCCAGAGATGATCAGAGCGGCGCCCTGCGAGCCGCC 51
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37  calaserValGlyGlyGlyGlyAlaSerSerProSer...AlaAlaA 53
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52  CGCTCTGTGGAGAGAGGTGGCGGCGCTCTCCCGCTCTGCAAGCGCTG 101
   |||||||
53  laAlaAlaAlaAlaAlaValSerSerSerAlaProGluIleValValSer 69
   |||||||
102  CGCGCGCGCGCGCGCTGTCCTTCACCCCGGAGATGCTGTCTCT 151
   |||||||
70  LysProGluHisAsnAsnSerAsnAsnLeuAlaLeuTYGlyThrGly 86
   |||||||
152  AAGCCCGAGCAACAACACTCCACACACTGCGCTGTATGAGACGCGCG 201
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86  yGlyGlySerThrGlyGlyGlyGlyGlyGlyGlySerGlyHisGly 103
   |||||||
202  CGGAGCGCAGCAGTGGAGAGCGGCGGCTGGCGGAGCGGAGCGCGCA 251
   |||||||
103  erSerSerGlyThrLysSerSerLysLysAsnGlnAsnIleGlyTyr 119
   |||||||
252  GCAGCAGTGCACCAAGTCCACAAAAGAAAACAGAACATCGCGTAC 301
   |||||||
120  LysLeuGlyHisArgArgAlaLeuPheGlyLysArgLysArgLysSer 136
   |||||||
302  AAGCTGGCGCCACCGCGCGCTGTTCCAAAAGCGCAAGCGCTCAGCGA 351
   |||||||
136  pTYrAlaLeuIlePheGlyMetPheGlyIleValValMetValIleGlu 153
   |||||||
352  CTACGGCGCTCATCTTGGCATGTGCGCATGTGTCATGTCATCGAGA 401

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153 hrgIuLeuSerTrpGlyValAlaTrpAspLysAlaSerLysLeuValAla 169
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402 CGGAGCTGGTGGTGGGCGCCCTACGACAAAGCTGCTATTCCTTAGCT 451
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170 LeuLysCysLeuIleSerLeuSer 177
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452 CTGAATGCTTATCATCATCTCTCC 475
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seq_name: gb_gss29:CNS01SOD

seq_documentation_block: 987 bp DNA GSS 12-MAY-2000
LOCUS CNS01SOD
DEFINITION Tetradon nigroviridis genome survey sequence T7 end of clone
170A18 of library G from tetradon nigroviridis, genomic survey
sequence.

ACCESSION AL165478.1 GI:7803216
VERSION AL165478
KEYWORDS GSS: genome survey sequence.
SOURCE Tetradon nigroviridis.
ORGANISM Tetradon nigroviridis
Chordata: Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Eurypterygii; Ctenosquamata; Acanthomorpha; Eucanthomorpha;
Holacanthopterygii; Acanthopterygii; Percormorpha;
Tetraodontiformes; Tetraodontidae; Tetraodontidae; Tetraodon.
1 (bases 1 to 987)
Roest-Crollius, H., Jallion, O., Dasilva, C., Fizes, C., Fisher, C.,
Bonneau, L., Billault, A., Queller, F., Saurin, W., Bernot, A. and
Weissenbach, J.

REFERENCE
AUTHORS Roest-Crollius, H., Jallion, O., Dasilva, C., Bonneau, L., Fisher, C.,
Bernot, A., Fizes, C., Wincker, P., Brothier, F., Queller, F.,
Saurin, W. and Weissenbach, J.
Human gene number estimate provided by genome wide analysis using
Tetradon nigroviridis DNA sequence

TITLE
Weissenbach, J.
Characterization and repeat analysis of the compact genome of the
freshwater pufferfish Tetradon nigroviridis

JOURNAL
AUTHORS Unpublished
2 (bases 1 to 987)
Roest-Crollius, H., Jallion, O., Dasilva, C., Bonneau, L., Fisher, C.,
Bernot, A., Fizes, C., Wincker, P., Brothier, F., Queller, F.,
Saurin, W. and Weissenbach, J.
Human gene number estimate provided by genome wide analysis using
Tetradon nigroviridis DNA sequence

REFERENCE
AUTHORS Unpublished
3 (bases 1 to 987)

JOURNAL
AUTHORS Direct Submission
Submitted (12-Apr-2000) to the EMBL/GenBank/DBJ databases
This sequence is a single read and was generated as part of a large
scale clone-end sequencing project of the Tetradon nigroviridis
genome. For more information, please take a look at
http://www.genoscope.cns.fr/Tetradon.

FEATURES
source Location/Qualifiers
1. 987
/organism="Tetradon nigroviridis"
/db_xref="taxon:99883"
/clone="170A18"
/clone_lib="G"
/note="Genoscope sequence ID : CGAG170BA091P1-end : 17"

BASE COUNT 277 a 247 c 240 g 217 t 6 others
ORIGIN

alignment_scores:
Quality: 747.00 Length: 291
Ratio: 3.735 Gaps: 5
Percent Similarity: 68.729 Percent Identity: 54.983

alignment_block:

US-09-254-590-19 x CNS01SOD/rev ..

Align seg 1/1 to reverse of: CNS01SOD from: 1 to: 987

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116 AsnIleGlyTyrLysLeuGlyHisArgArgAlaLeuPheGlyLysArg 132
   |||||||
985 GATATCGGCTACGCTGCGCGCAGAGAAAGCTCTTGTG...AAGCCAA 939
   |||||||

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308 GTCGAGAGCATTATAGCAAGTGAAGTCTCTGATTTATCAATATA 357
162 ..... 162
358 AATCTTAGCTTCTGATTAACATCCGTGATTCACAACTAGAGTTG 407
163 .....Ala.SerLeuTyrSerLeuA 169
408 TCTCAATATKCTGTCTTCATTTCTCTAGGAATTCGTATATTGACAG 457
169 IaleuLysCysLeuIleSerLeuSerThrIleIleLeuLeuGlyLeuIle 185
458 TKCTAAAGGCGCTGATCAGTCTTCCAGCGCTGTCTCTGTGTTCTAATT 507
186 ILeValTyrHisAlaIArgGlu..... 192
508 GTKATGTACCATGACAGGGAAATTCAGGCACTGGACAAAGGACCATA 557
192 ..... 192
558 GGAATCTATTAGATATKAGACACCAACTCTCCCTGAATGATCA 607
193 .....Ile.GlnLeuPheMetValAspAsnGlyAl 202
608 GTGAAGTTCTCTCTCTTCTTCTGACAGCTGTTCATGTGACAAAGTGC 657
202 AASPAPPTPARGIleAlaMetThrTyrGlnArgIlePhePheIleCysL 219
658 AGAGACTGAGAGATAGCTATGACTTTGAGCGGATTCCTTTGTCTGCC 707
219 eugluIleLeuValCysAlaIleHisProIleProGlyAsnTyrThrPhe 235
708 TGGAGCTCTCTGCTGCKCATCCATCCGCTCCAGGCCAATACGTCTTC 757
236 ThrTriPThrAlaArgLeuAlaPheSerTyrAlaProSerThrThrAl 252
758 AGCTGGACCAACCCGCTGTGCCCGCACTACACGCGGGGCGCTGAGACG 807
252 aaspValAspIleIleLeuSerIleProMetPheLeuArgLeuTyrLeuI 269
808 TGACGTGAGACTCATCTCTCTGCGCATGTCTCGCGCTCTACTGA 857
269 leAlaArgValMetLeuLeuHisSerLysLeuPheThrAspAlaSerSer 285
858 TTGGCCGGGTGATGTGCTCCACAGCAAGCTCTTACCGACGCTTCTCC 907
286 ArgSerIleGlyAlaLeuAsnLysIleAsnPheAsnThrArgPheValMe 302
908 CGCAGCATCGGGGCTCAACAGATCAGCTTAKACACTCKCTTCTGAT 957
302 tLysThrLeuMetThrIleCysProGlyThrValLeuLeuValPheSerI 319
958 GAAGACGCTGATGACCATTCGCCGTGATGCTCTGTCTTACGG 1007
319 leSerLeuTriP 322
1008 TGACCCGCTGG 1018

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•
•

GenCore version 4.5
Copyright (c) 1993 - 2000 Compen Ltd.

OM protein - protein search, using sw model

Run on: May 14, 2001, 18:47:21 ; Search time 51.95 Seconds
(without alignments)
1306.321 Million cell updates/sec

Title: US-09-254-590-19
Perfect score: 2954
Sequence: 1 MSSCRNGVWRPPLSNLSAS.....SSRRRRSSSTAPPSSSS 579

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 374700 seqs, 117207915 residues

Total number of hits satisfying chosen parameters: 374700

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPREMBL.15:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_oranella:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_unclassified:*
13: sp_vertebrate:*
14: sp_virus:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	2893.5	98.0	580	11 P70604	P70604 rattus norv
2	2638	89.3	553	13 O9PNS9	O9PNS9 gallus gall
3	2125.5	72.0	736	4 O9UGT6	O9UGT6 homo sapien
4	2121.5	71.8	732	11 P70605	P70605 rattus norv
5	2118.5	71.7	731	4 O43517	O43517 homo sapien
6	1868.5	63.3	561	4 O92952	O92952 homo sapien
7	1779.5	60.2	536	11 P70606	P70606 rattus norv
8	997	33.8	907	5 O19186	O19186 caenorhabdi
9	902	30.5	925	5 O9XTJ3	O9XTJ3 caenorhabdi
10	894.5	30.3	425	11 O9WV45	O9WV45 rattus norv
11	893.5	30.2	425	11 O89109	O89109 mus musculu
12	890.5	30.1	425	11 O9OYWI	O9OYWI rattus norv
13	886.5	30.0	424	11 O9RI98	O9RI98 rattus norv
14	880.5	29.8	427	4 O15554	O15554 homo sapien
15	871.7	24.3	156	5 O9W4C7	O9W4C7 drosophila
16	683.5	23.1	282	5 O9W4C6	O9W4C6 drosophila
17	532.5	18.0	475	5 O17697	O17697 caenorhabdi
18	204.5	6.9	932	4 O9NR82	O9NR82 homo sapien
19	188	6.4	908	5 O18476	O18476 loligo peal

20	182	6.2	897	4 O9NRN0	O9NRN0 homo sapien
21	179	6.1	878	11 O9JRX45	O9JRX45 mus musculu
22	165.5	5.6	861	4 O9NIX36	O9NIX36 homo sapien
23	163	5.5	873	11 O88944	O88944 rattus norv
24	161.5	5.5	514	5 O76457	O76457 aplysia cal
25	160	5.4	1175	6 O9TV66	O9TV66 oryctolagus
26	156.5	5.3	393	4 O99454	O99454 homo sapien
27	156.5	5.3	570	11 O92347	O92347 mus musculu
28	155.5	5.3	463	11 O92344	O92344 mus musculu
29	155.5	5.3	723	11 O92348	O92348 mus musculu
30	155.5	5.3	747	11 O92349	O92349 mus musculu
31	155.5	5.3	754	11 O92350	O92350 mus musculu
32	155.5	5.3	759	11 O92351	O92351 mus musculu
33	154.5	5.2	841	4 O95845	O95845 homo sapien
34	154.5	5.2	852	11 O88943	O88943 rattus norv
35	154.5	5.2	854	4 O75580	O75580 homo sapien
36	153.5	5.2	473	11 O92345	O92345 mus musculu
37	153.5	5.2	623	11 O92346	O92346 mus musculu
38	153.5	5.2	623	11 O92346	O92346 mus musculu
39	151.5	5.1	744	5 O18147	O18147 caenorhabdi
40	151	5.1	1178	4 O13150	O13150 homo sapien
41	151	5.1	1178	4 O12960	O12960 homo sapien
42	150	5.1	835	11 O92240	O92240 rattus norv
43	150	5.1	1210	11 O9WU13	O9WU13 rattus norv
44	150	5.1	1243	11 O55180	O55180 rattus norv
45	148.5	5.0	872	4 O43526	O43526 homo sapien

ALIGNMENTS

RESULT	1	PRELIMINARY:	PRT:	580 AA.
ID	P70604			
AC	P70604:			
DT	01-FEB-1997 (TREMURel. 02, Created)			
DT	01-FEB-1997 (TREMURel. 02, Last sequence update)			
DT	01-JUN-2000 (TREMURel. 14, Last annotation update)			
DE	CALCIUM-ACTIVATED POTASSIUM CHANNEL NSK2.			
OS	Rattus norvegicus (Rat).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.			
OX	NCBI_TaxID=10116;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=SPRAGUE-DAWLEY; TISSUE=BRAIN;			
RA	MEDLINE=96376602; PubMed-8781233;			
RA	Kohler M., Hirschberg B., Bond C.T., Kinzie J.M., Marston N.V.,			
RA	Maylie J., Adelman J.P.;			
RT	"Small-conductance, calcium-activated potassium channels from			
RT	mammalian brain."			
RL	Science 273:1709-1714 (1996).			
DR	EMBL: U69882; AAB09563.1; .			
DR	INTERPRO: IPR001622; .			
KW	Ionic channel.			
SQ	SEQUENCE 580 AA; 63847 MW; F71E0DAF7EEFA8D4 CRC64;			

Query Match 98.0%; Score 2893.5; DB 11; Length 580;

Best local similarity 97.9%; Pred. No. 2.2e-197;
Matches 572; Conservative 1; Indels 9; Gaps 3;

OY	1	MSSCRNGVWRPPLSNLSASRRNLEHMSKOPLOPPAS-VGGGGGASSPSAAAAAANV	59
DB	1	MSSCRNGVWRPPLSNLSASRRNLEHMSKOPLOPPASVGGGGGASSPSAAAAAANV	56
OY	60	SSSAPEIVVSKPEHNNNNLALYGTGGGGSST---GGGGGGGGSGHSSSGTSSKKKKQ	115
DB	57	SSSAPEIVVSKPEHNNNNLALYGTGGGGSSTGGGGGGGGGGSSSGTSSKKKKQ	116
OY	116	NGCYLGHRRRLFEKKRRLSDVALFEFGFIVVWVIEFELISGAVADKASLYSLALCLIS	175
DB	117	NGCYLGHRRRLFEKKRRLSDVALFEFGFIVVWVIEFELISGAVADKASLYSLALCLIS	176

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QY 176 LSTIILGLIIVYHAREIOLFVWDGADDMRIAMTERIEFTCLEILVCAIHPICNTYF 235
DB 177 LSTIILGLIIVYHAREIOLFVWDGADDMRIAMTERIEFTCLEILVCAIHPICNTYF 236
QY 236 TWTARLAFSAVSTTADVDIILSIIPMFLRLYLARVMLHLSKLETDASSRIGALINKIN 295
DB 237 TWTARLAFSAVSTTADVDIILSIIPMFLRLYLARVMLHLSKLETDASSRIGALINKIN 296
QY 296 FNTFRVMTLMTCPGVLLVFSISLMTIAAMTVRACERYHDOODVTSNFGAMMLISIT 355
DB 297 FNTFRVMTLMTCPGVLLVFSISLMTIAAMTVRACERYHDOODVTSNFGAMMLISIT 356
QY 356 FLISIGDMPVNTYCGKVCCLTIGMAGCTALVAVVARKLETKAEKHVHNFMDTOL 415
DB 357 FLISIGDMPVNTYCGKVCCLTIGMAGCTALVAVVARKLETKAEKHVHNFMDTOL 416
QY 416 TKRYNMAANVLRFTWLYKNTKLYKKIDAKVRKHQKFLQAIHOLRSVKMEORLANDQ 475
DB 417 TKRYNMAANVLRFTWLYKNTKLYKKIDAKVRKHQKFLQAIHOLRSVKMEORLANDQ 476
QY 476 ANTLVDLAKTONIMYDMSIDNERSDEFEKRIYVLETKLETLIGSIHALPGLISOTIROQ 535
DB 477 ANTLVDLAKTONIMYDMSIDNERSDEFEKRIYVLETKLETLIGSIHALPGLISOTIROQ 536
QY 536 QHDFEAMQESYDKHVTYNAERSRSSRRSSSTAPPTSSSS 579
DB 537 QHDFEAMQESYDKHVTYNAERSRSSRRSSSTAPPTSSSS 580

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RESULT 2

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Q9PTS9 PRELIMINARY: PRT: 553 AA.
ID 09PTS9
AC 09PTS9
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TREMBLrel. 14, Last annotation update)
DE SMALL-CONDUCTANCE CALCIUM-ACTIVATED POTASSIUM CHANNEL.
GN SK2.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RA Zidanic M., Fuchs P.A.;
RT "Small conductance calcium-activated potassium channel expressed in
RT chick cochlear hair cells.";
RL EMBL: AF079372; AAF21783.1;
DR EMBL: AF079372; AAF21783.1;
DR INTERPRO: IPR001622;
KW Ionic channel.
SQ SEQUENCE 553 AA: 62016 MW: AE7D493EAE11074A CRC64;

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Query Match 89.3%; Score 2638; DB 13; Length 553;
 Best Local Similarity 90.5%; Pred. No. 2,8e-179;
 Matches 524; Conservative 12; Mismatches 17; Indels 26; Gaps 4;

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QY 1 MSSCRNGGVMPRLSNLSASRRNLHMDSEAOPLPPASVGGGGGASPSMAAANAAYS 60
DB 1 MSSCRNGGVMPRLSNLSASRRNLHMDSEAOPLPPASVGGGGGASPSMAAANAAYS 60
QY 61 SSAPETLYVSKPEHNNNSNNLALYGTGGGSGTGGGGSGSGSSGTSKSKKNONIGYK 120
DB 61 SSAPETLYVSKPEHNNNSNNLALYGTGGGSGTGGGGSGSGSSGTSKSKKNONIGYK 120
QY 45 --GPEYVYVSKPEHNNNSNNLALYGPAGPGP-----GPGGPNNG---GTPKTKKNNONIGYK 94
DB 45 --GPEYVYVSKPEHNNNSNNLALYGPAGPGP-----GPGGPNNG---GTPKTKKNNONIGYK 94
QY 121 LGHRRALFEKRRRLSDYALIFGMEGIVVYVETELSGVADKASLYSLALCLISSTII 180
DB 121 LGHRRALFEKRRRLSDYALIFGMEGIVVYVETELSGVADKASLYSLALCLISSTII 180
QY 95 LGHRRALFEKRRRLSDYALIFGMEGIVVYVETELSGVADKASLYSLALCLISSTII 154
DB 95 LGHRRALFEKRRRLSDYALIFGMEGIVVYVETELSGVADKASLYSLALCLISSTII 154
QY 181 LGLIIVYHAREIOLFVWDGADDMRIAMTERIEFTCLEILVCAIHPICNTYFTW 240
DB 181 LGLIIVYHAREIOLFVWDGADDMRIAMTERIEFTCLEILVCAIHPICNTYFTW 240

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DB 155 LGLIIVYHAREIOLFVWDGADDMRIAMTERIEFTCLEILVCAIHPICNTYFTW 214
QY 241 LAFSAVSTTADVDIILSIIPMFLRLYLARVMLHLSKLETDASSRIGALINKIN 300
DB 215 LAFSAVSTTADVDIILSIIPMFLRLYLARVMLHLSKLETDASSRIGALINKIN 274
QY 301 VAKTLMTCIPGVLLVFSISLMTIAAMTVRACERYHDOODVTSNFGAMMLISIT 360
DB 275 VAKTLMTCIPGVLLVFSISLMTIAAMTVRACERYHDOODVTSNFGAMMLISIT 334
QY 361 YGDMPVNTYCGKVCCLTIGMAGCTALVAVVARKLETKAEKHVHNFMDTOLTKRVK 420
DB 335 YGDMPVNTYCGKVCCLTIGMAGCTALVAVVARKLETKAEKHVHNFMDTOLTKRVK 394
QY 421 NNAANVLRFTWLYKNTKLYKKIDAKVRKHQKFLQAIHOLRSVKMEORLANDQ 480
DB 395 NNAANVLRFTWLYKNTKLYKKIDAKVRKHQKFLQAIHOLRSVKMEORLANDQ 454
QY 481 DLAKTONIMYDMSIDNERSDEFEKRIYVLETKLETLIGSIHALPGLISOTIROQ 540
DB 455 DLAKTONIMYDMSIDNERSDEFEKRIYVLETKLETLIGSIHALPGLISOTIROQ 514
QY 541 EAQMESYDKHVTYNAERSRSSRRSSSTAPPTSSSS 579
DB 515 EAQMESYDKHVTYNAERSRSSRRSSSTAPPTSSSS 553

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RESULT 3

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Q9UGT6 PRELIMINARY: PRT: 736 AA.
ID 09UGT6
AC 09UGT6
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TREMBLrel. 14, Last annotation update)
DE SK3 PROTEIN.
GN K3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Terstappen G.C., Pula G., Chen M.X., Roncarati R.;
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AJ251016; CAB61331.1;
DR INTERPRO: IPR001622;
SQ SEQUENCE 736 AA: 82025 MW: CCD0CC1621FFAB9C CRC64;

```

Query Match 72.0%; Score 2125.5; DB 4; Length 736;
 Best Local Similarity 73.2%; Pred. No. 9.5e-143;
 Matches 428; Conservative 48; Mismatches 72; Indels 37; Gaps 4;

```

QY 1 MSSCRNGGVMPRLSNLSASRRNLHMDSEAOPLPPASVGGGGGASPSMAAANAAYS 60
DB 180 MSSCRNGGVMPRLSNLSASRRNLHMDSEAOPLPPASVGGGGGASPSMAAANAAYS 218
QY 61 SSAPETLYVSKPEHNNNSNNLALYGTGGGSGTGGGGSGSGSSGTSKSKKNONIGYK 114
DB 219 SNPEYVYVSKPEHNNNSNNLALYGTGGGSGTGGGGSGSGSSGTSKSKKNONIGYK 268
QY 115 QNIGYKLGHRALFEKRRRLSDYALIFGMEGIVVYVETELSGVADKASLYSLALCLIS 174
DB 269 QNIGYKLGHRALFEKRRRLSDYALIFGMEGIVVYVETELSGVADKASLYSLALCLIS 328
QY 175 SUSTIILGLIIVYHAREIOLFVWDGADDMRIAMTERIEFTCLEILVCAIHPICNTY 234
DB 329 SUSTIILGLIIVYHAREIOLFVWDGADDMRIAMTERIEFTCLEILVCAIHPICNTY 388
QY 235 FWTARLAFSAVSTTADVDIILSIIPMFLRLYLARVMLHLSKLETDASSRIGALINKI 294
DB 389 FWTARLAFSAVSTTADVDIILSIIPMFLRLYLARVMLHLSKLETDASSRIGALINKI 448

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QY 295 NFNTRFVMTLMTICPGTVLLVFSISLWIIAAMVACERYHDOOVYNSNFGAMWLISI 354
DB 449 NFNTRFVMTLMTICPGTVLLVFSISLWIIAAMVACERYHDOOVYNSNFGAMWLISI 508
QY 355 TFLSIGDGVNPTVCGKVCCLTGLMGAGCTALVAVVARKLELTKAEKHHVNMMDTQ 414
DB 509 TFLSIGDGVNPTVCGKVCCLTGLMGAGCTALVAVVARKLELTKAEKHHVNMMDTQ 568
QY 415 LTRKVKAAANVLRRETLVYKNTLYKTKIDHAKVRRHOKFLQAIHQLSVYKMEQRKLD 474
DB 569 LTRKVKAAANVLRRETLVYKNTLYKTKIDHAKVRRHOKFLQAIHQLSVYKMEQRKLD 628
QY 475 QANTLVDAKTONIMYDMSDLNRSSEDFEKRIVTLETKETLIGSIHALPGLISQTIQ 534
DB 629 QANTLVDSKQVMVYDITELNDRSEDEKQIGSLESKEHLTASPNISPLLIADTLRQ 688
QY 535 QORDFEAOESYDKHVTYNAERSRRSSRRSSSTAPTSSESS 579
DB 689 QOQOLITAEVARGISVAVGTSHAPSDSPDIGISTSEPTPTYS 729

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RESULT 4
P70605 PRELIMINARY: PRT: 732 AA.
ID P70605:
AC 01-FEB-1997 (Tremblrel. 02, Created)
DT 01-FEB-1997 (Tremblrel. 02, last sequence update)
DY 01-JUN-2000 (Tremblrel. 14, last annotation update)
DE CALCIUM-ACTIVATED POTASSIUM CHANNEL RSK3.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RS SEQUENCE FROM N.A.
RC STRAIN=SPRAGUE-DAWLEY; TISSUE=BRAIN;
RX MEDLINE=96376602; PubMed=8781233;
RA Kohler M., Hirschberg B., Bond C.F., Kinzie J.M., Marrion N.V.,
Maylie J., Adelman J.P.;
RT "Small-conductance, calcium-activated potassium channels from
mammalian brain.";
RL Science 273:1709-1714(1996).
DR EMBL: U69884; AAB81653.1; -.
DR INTERPRO: IPR001622; -.
KW Ionic channel.
FT DOMAIN 30 35 POLY-GLN.
FT DOMAIN 36 39 POLY-PRO.
FT DOMAIN 60 80 POLY-GLN.
FT DOMAIN 684 688 POLY-GLN.
FT DOMAIN 728 731 POLY-SER.
SQ SEQUENCE 732 AA; 81447 MW; 9EDB52926EA7BD6C CRC64;

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Query Match 71.8%; Score 2121.5; DB 11; Length 732;
 Best Local Similarity 72.8%; Pred. No. 1.8e-142;
 Matches 426; Conservative 49; Mismatches 73; Indels 37; Gaps 4;

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QY 1 MSCRYNGVMPRLSNLSASRRNLHEMDEAPDIPPAVSAGGGGSGSSPSAAAAAAYS 60
DB 176 MSCRYSGVMPRLSNLSASRRNLHEMDEAPDIPPAVSAGGGGSGSSPSAAAAAAYS 214
QY 61 SSAPEIYVSKPEHNHNNALVGTG-----GGSTGGGGGGSGSSGSSSTKSKKN 114
DB 215 SNPEIYSSREDNNAHOTLLHHPNATHNHQHGCTA-----GSTPEPKANKKN 264
QY 115 ONIGKIGHRALFEKRRKLSYALITGMCYVWVITELSMGADYKSLAKLCLISLSTII 174
DB 265 ONIGKIGHRALFEKRRKLSYALITGMCYVWVITELSMGADYKSLAKLCLISLSTII 324
QY 175 LGLIIVYHARETOLEFVNDGADDMRIAMTERIFELTLCALVCAHPITPTWJAR 234
DB 325 LGLIIVYHARETOLEFVNDGADDMRIAMTERIFELTLCALVCAHPITPTWJAR 384

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QY 235 FYTARLASVAPSTTADVDIILSTPMFLRYLIARVMLJHSKLEPTDASSRIGALNKI 294
DB 385 FYTARLASVAPSTTADVDIILSTPMFLRYLIARVMLJHSKLEPTDASSRIGALNKI 444
QY 295 NFNTRFVMTLMTICPGTVLLVFSISLWIIAAMVACERYHDOOVYNSNFGAMWLISI 354
DB 449 NFNTRFVMTLMTICPGTVLLVFSISLWIIAAMVACERYHDOOVYNSNFGAMWLISI 504
QY 355 TFLSIGDGVNPTVCGKVCCLTGLMGAGCTALVAVVARKLELTKAEKHHVNMMDTQ 414
DB 509 TFLSIGDGVNPTVCGKVCCLTGLMGAGCTALVAVVARKLELTKAEKHHVNMMDTQ 564
QY 415 LTRKVKAAANVLRRETLVYKNTLYKTKIDHAKVRRHOKFLQAIHQLSVYKMEQRKLD 474
DB 569 LTRKVKAAANVLRRETLVYKNTLYKTKIDHAKVRRHOKFLQAIHQLSVYKMEQRKLD 624
QY 475 QANTLVDAKTONIMYDMSDLNRSSEDFEKRIVTLETKETLIGSIHALPGLISQTIQ 534
DB 629 QANTLVDSKQVMVYDITELNDRSEDEKQIGSLESKEHLTASPNISPLLIADTLRQ 684
QY 535 QORDFEAOESYDKHVTYNAERSRRSSRRSSSTAPTSSESS 579
DB 689 QOQOLITAEVARGISVAVGTSHAPSDSPDIGISTSEPTPTYS 729

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RESULT 5
O43517 PRELIMINARY: PRT: 731 AA.
ID O43517:
AC 01-JUN-1998 (Tremblrel. 06, Created)
DT 01-NOV-1998 (Tremblrel. 08, last sequence update)
DY 01-JUN-2000 (Tremblrel. 14, last annotation update)
DE CALCIUM-ACTIVATED POTASSIUM CHANNEL.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RS SEQUENCE FROM N.A.
RA Chandry K.G., Fantlino E., Wittekindt O., Kalman K., Tong L.-L.,
Ho T.-H., Gutman G.A., Croc M.-A., Ganguli R., Nimgaonkar V.,
Morris-Rosendahl D.J., Gargus J.J.;
RT "Isolation of a novel potassium channel gene hSKCa3 containing a
polymorphic CAG repeat: a candidate for schizophrenia and bipolar
disorder?";
RL Mol. Psych. 3:32-37(1998).
DR EMBL: AF031815; AAC26099.1; -.
DR INTERPRO: IPR001622; -.
KW Ionic channel.
SQ SEQUENCE 731 AA; 81282 MW; CA12AC23865124DE CRC64;

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Query Match 71.7%; Score 2118.5; DB 4; Length 731;
 Best Local Similarity 73.7%; Pred. No. 2.9e-142;
 Matches 427; Conservative 48; Mismatches 79; Indels 25; Gaps 3;

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QY 1 MSCRYNGVMPRLSNLSASRRNLHEMDEAPDIPPAVSAGGGGSGSSPSAAAAAAYS 60
DB 175 MSCRYSGVMPRLSNLSASRRNLHEMDEAPDIPPAVSAGGGGSGSSPSAAAAAAYS 213
QY 61 SSAPEIYVSKPEHNHNNALVGTG-----GGSTGGGGGGSGSSGSSSTKSKKNONIGY 120
DB 214 SNPEIYSSREDNNAHOTLLHHPNATHNHQHGCTA-----GSTPEPKANKKNONIGY 269
QY 121 LGHRRALFEKRRKLSYALITGMCYVWVITELSMGADYKSLAKLCLISLSTII 180
DB 270 LGHRRALFEKRRKLSYALITGMCYVWVITELSMGADYKSLAKLCLISLSTII 329
QY 181 LGLIIVYHARETOLEFVNDGADDMRIAMTERIFELTLCALVCAHPITPTWJAR 240
DB 330 LGLIIVYHARETOLEFVNDGADDMRIAMTERIFELTLCALVCAHPITPTWJAR 389

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QY 241 LAFSVASTTTADVDTIIISTIPMFLRLYLARVWMLHSLKLTDDASSRSIGALNKINENTRE 300
DB 390 LAFTSTPSRAEADVDTIIISTIPMFLRLYLARVWMLHSLKLTDDASSRSIGALNKINENTRE 449
QY 301 VMKTLMTICPGVLLVFSISLMTIAAMTVACERYHDQDVTNFIAGAMWLSTIFLSIG 360
DB 450 VMKTLMTICPGVLLVFSISLMTIAAMTVACERYHDQDVTNFIAGAMWLSTIFLSIG 509
QY 361 YGDMVPNTYCGKVCCLLTGIMGACCTALVAVVARKLETLKAEKHYHNMMDTOLTKRK 420
DB 510 YGDMVPNTYCGKVCCLLTGIMGACCTALVAVVARKLETLKAEKHYHNMMDTOLTKRK 569
QY 421 NAAANVRETWLLIYKNTLVKIDHAKVRRKORFLQAIHQLSRYKGEORLKNQDAMTV 480
DB 570 NAAANVRETWLLIYKNTLVKIDHAKVRRKORFLQAIHQLSRYKGEORLKNQDAMTV 629
QY 481 DLAKTONIMYDMISDLNRSDEPKRIYTLTKETLTLGSIHALPGLISQITRQOQDFT 540
DB 630 DLAKTONIMYDMISDLNRSDEPKRIYTLTKETLTLGSIHALPGLISQITRQOQDFT 589
QY 541 EAQMSYDKHVTYNAENSRSSRRSSSTAPPTSSBS 579
DB 690 SALLERGVSAVGTHTHTPISDSPIGVSTSPPTSS 728

RESULT 6
QY 092952 PRELIMINARY: PRT: 561 AA.
AC 092952:
DT 01-FEB-1997 (TREMblrel. 02, Created)
DT 01-FEB-1997 (TREMblrel. 02, Last sequence update)
DT 01-JUN-2000 (TREMblrel. 14, Last annotation update)
DE CALCIUM-ACTIVATED POTASSIUM CHANNEL HSK1.
GN SK OR KCNN1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=BRAIN;
RX MEDLINE=96376602; PubMed=8781233;
RA Kohler M., Hirschberg B., Bond C.T., Kinzie J.M., Marrión N.V.,
RA Maylie J., Adelman J.P.;
RT "Small-conductance, calcium-activated potassium channels from
RT mammalian brain.";
RL Science 273:1709-1714(1996).
RN [2]
RP SEQUENCE FROM N.A.
RA Litt M., Lamorticella D.M., Bond C.T., Adelman J.P.;
RT "Gene structure and chromosomal mapping of the human small-conductance
RT calcium-activated potassium channel gene hsk1 (KCNN1).";
RL Cytogenet. Cell Genet. 0:0-0(1999).
DR EMBL: U69883; AAB09562.1; -
DR EMBL: AF131948; AAD37507.1; -
DR EMBL: AF131940; AAD37507.1; JOINED.
DR EMBL: AF131941; AAD37507.1; JOINED.
DR EMBL: AF131942; AAD37507.1; JOINED.
DR EMBL: AF131943; AAD37507.1; JOINED.
DR EMBL: AF131944; AAD37507.1; JOINED.
DR EMBL: AF131945; AAD37507.1; JOINED.
DR EMBL: AF131946; AAD37507.1; JOINED.
DR EMBL: AF131947; AAD37507.1; JOINED.
DR INTERPRO: IPR001622; -
KW Ionic channel.
SQ SEQUENCE 561 AA: 61826 MW: 66CA9A21C5FFDE74 CRC64;

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Query Match 63.3%; Score 1868.5; DB 4; Length 561;
 Best Local Similarity 70.3%; Pred. No. 1,2e-124;
 Matches 378; Conservative 46; Mismatches 79; Indels 35; Gaps 7;

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QY 1 MSSCRVNGVMPRL-SNLASRNLEHMDSEA-QPLPPASVGGGGGAGSSPAAAAAAA 58
DB 19 MNSHYNIGSVGRPLSGALGR--PPDEAGHPQGPSPG-----LQVYVAKSEPAR 71
QY 59 VSSAPEIVVSRPEHNNNSNNLALYGTGGGGTGGGGGGSSGSSGSSKSKKKNONIG 118
DB 72 PPSGSPR--GQPOQDDDE-----DDEEDBAGHORSKPSNVG 108
QY 119 YKGRHRALEFEKRLSDYALITGMGYVWYIETELSMGADYKASLSLAKCLISLT 178
DB 109 HRGHRRALEFEKRLSDYALITGMGYVWYIETELSMGADYKASLSLAKCLISLT 168
QY 179 ILLGLIIVYHARETOLFMVNDGADDMRIAMTYERIFLCTLVCAIHPPIGMYPTMT 238
DB 169 AILGLVLYVYHARETOLFMVNDGADDMRIAMTYERIFLCTLVCAIHPPIGMYPTMT 228
QY 239 ARLAFSVASTTTADVDTIIISTIPMFLRLYLARVWMLHSLKLTDDASSRSIGALNKINENT 298
DB 229 ARLAFSVASTTTADVDTIIISTIPMFLRLYLARVWMLHSLKLTDDASSRSIGALNKINENT 288
QY 299 REVMKTLMTICPGVLLVFSISLMTIAAMTVACERYHDQDVTNFIAGAMWLSTIFLS 358
DB 289 REVMKTLMTICPGVLLVFSISLMTIAAMTVACERYHDQDVTNFIAGAMWLSTIFLS 348
QY 359 IGYDMVPNTYCGKVCCLLTGIMGACCTALVAVVARKLETLKAEKHYHNMMDTOLTKR 418
DB 349 IGYDMVPNTYCGKVCCLLTGIMGACCTALVAVVARKLETLKAEKHYHNMMDTOLTKR 408
QY 419 VKNAAANVRETWLLIYKNTLVKIDHAKVRRKORFLQAIHQ--LRSYKMDQRKNDQ 475
DB 409 VKNAAANVRETWLLIYKNTLVKIDHAKVRRKORFLQAIHQ--LRSYKMDQRKNDQ 468
QY 476 ANTLVDLAKTONIMYDMISDLNRSDEPKRIYTLTKETLTLGSIHALPGLISQITR 533
DB 469 ANTLVDLAKTONIMYDMISDLNRSDEPKRIYTLTKETLTLGSIHALPGLISQITR 526

RESULT 7
QY P70606 PRELIMINARY: PRT: 536 AA.
AC P70606:
DT 01-FEB-1997 (TREMblrel. 02, Created)
DT 01-NOV-1998 (TREMblrel. 08, Last sequence update)
DT 01-JUN-2000 (TREMblrel. 14, Last annotation update)
DE CALCIUM-ACTIVATED POTASSIUM CHANNEL RSK1.
GN Rattus norvegicus (Rat).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=BRAIN;
RX MEDLINE=97454570;
RA Joiner W.J., Wang L.Y., Tang M.D., Kaczmarek L.K.;
RA Proc. Natl. Acad. Sci. U.S.A. 94:11013-11018(1997).
RN [2]
RP SEQUENCE OF 79-536 FROM N.A.
RC STRAIN=SPRAGUE-DAWLEY; TISSUE=BRAIN;
RX MEDLINE=96376602; PubMed=8781233;
RA Kohler M., Hirschberg B., Bond C.T., Kinzie J.M., Marrión N.V.,
RA Maylie J., Adelman J.P.;
RT "Small-conductance, calcium-activated potassium channels from
RT mammalian brain.";
RL Science 273:1709-1714(1996).
DR EMBL: AF000973; AAB82740.1; -
DR EMBL: U69885; AAB09564.1; -
DR INTERPRO: IPR001622; -
KW Ionic channel.
SQ SEQUENCE 536 AA: 59214 MW: 97FE02071B0B36A CRC64;

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Query Match 60.2%; Score 1779.5; DB 11; Length 536;

Tue May 15 08:41:28 2001

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Page 5

Best Local Similarity 66.4%; Pred. No. 2,3e-118;
Matches 360; Conservative 49; Mismatches 84; Indels 49; Gaps 6;

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QY 1 MSSCRNGVMPRLNLSASRRNLHEDSEA-QPLQPPASV-----GGGSSPSMAA 53
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 MSSRSHNGSVGRPLS-GPGFLGWEVPDPAEPQPPQPGGLQMAKQPGALSPSPR 59
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 54 AAAAAVSSAPELVSKPEHNNSNNLALYGTGGGGSTGGGGGGSGHSSGSSSTKSKK 113
    :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 60 GHQAQEEDEDEDEDEP-----GSG-----K 81
QY 114 NONIGYKLGHRRLAFKRRRLSDYALFGMGIVVWVETELSMGADKALYSIALKCL 173
    :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 82 PPTVSHRGLGHRRLAFKRRRLSDYALFGMGIVVWVETELSMGADKALYSIALKCL 141
    :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 174 ISLSTILLGLIYVHAREIOLFWYDNGADDMRIAMTERIERIFICELVCAIHPIPGNY 233
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 142 ISLSTILLGLIYVHAREIOLFWYDNGADDMRIAMTERIERISLELAVALHPVGHY 201
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 234 TFWTARLAFSTAPSTTADVDIISIPWFLRLYLARVMLHSLKFTDASSRIGALNK 293
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 202 RFTWTRALFSLVSPAADVDYLSIPWFLRLYLARVMLHSLKFTDASSRIGALNK 261
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 294 INFNTREFVMTKLTICPGTVLVFSSIMTIAAVTRACERHDDQDVTSNGLAMWLIS 353
    :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 262 VTFNTRFVMTKLTICPGTVLVFSSIMTIAAVTRACERHDDQDVTSNGLAMWLIS 321
    :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 354 ITFLSTIGYDMVNPYTCGKGYCLLTGIMGAGCTALVAVAVARKLELTKAKKHYHNMMDT 413
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 322 ITFLSTIGYDMVNPYTCGKGYCLLTGIMGAGCTALVAVAVARKLELTKAKKHYHNMMDT 381
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 414 QLTREKVNAAANVLRKRWLYKNTLVKIDHAKVRRHOKRFLQAIHQ---LRSYMER 470
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 382 QLTREKVNAAANVLRKRWLYKNTLVKIDHAKVRRHOKRFLQAIHQ---LRSYMER 441
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 471 KLNDQANTLVLDLAKTONIMYDMSIDNRSDEPKRYVLETKETLGLSIHALPGLSIQ 530
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 442 KLNDQANTLVLDLAKTONIMYDMSIDNRSDEPKRYVLETKETLGLSIHALPGLSIQ 501
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 531 TT 532
    :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 502 AT 503
    :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
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Query Match 33.8%; Score 997; DB 5; Length 907;
Best Local Similarity 40.1%; Pred. No. 1.5e-62; Indels 92; Gaps 11;
Matches 226; Conservative 88; Mismatches 157;

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QY 36 PPASVGGGGGASSPSMAAANVSSAPELVSK-----PEHNNSNNL-----ALYK 83
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 357 PVFAVSGGGGGS-----CAVSPSSARKREPSKWRSLDKORSSESMERNEDHELIA 409
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 84 TGGG-----GSGT----- 100
    :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 410 DGRMRMAYLPREGQALRLRILGPOGLSWISHRETRAKSVSIAYNDLGAAGKNGCA 469
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 101 HSSSGTKSSKKNQONIGYKLGHRRLAFKRRRLSDYALFGMGIVVWVETELSMGAY 160
    :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 470 IDDDSTVPLMDKDNSSGRLRRLREIHKRRHVSRLAALALINGITLITENELR-TAY 528
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 161 --DKASLYSLAKCLISLSTILLGLIYVHAREIOLFWYDNGADDMRIAMTERIERIFIC 588
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 529 VIRPGSSLSHLKFFIETTLALSFVGFVHVEIQLFNNANAAADMMVWVLSRRTCQIG 588
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 219 LFTVCAHPIPIPGVTFWTARLAFSVAP-----STTADVDIISIPWFLRLYLAR 271
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 589 LFTVCAHPIPIPGVTFWTARLAFSVAP-----STTADVDIISIPWFLRLYLAR 271
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 272 VMLHSLKFTDASSRIGALNKINFNTREFVMTKLTICPGTVLVFSSIMTIAAVTR 331
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 638 VMLHSLKFTDASSRIGALNKINFNTREFVMTKLTICPGTVLVFSSIMTIAAVTR 309
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 332 CERHDDQDVTS--NFLGAMWLISITFLSTIGYDMVNPYTCGKGYCLLTGIMGAGCTALV 389
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 698 CERHDDQDVTS--NFLGAMWLISITFLSTIGYDMVNPYTCGKGYCLLTGIMGAGCTALV 357
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 390 VAVYVARKLELTKAKKHYHNMMDTQTLRKVNAAANVLRKRWLYKNTLVKIDHAKV 449
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 758 VAVYVARKLELTKAKKHYHNMMDTQTLRKVNAAANVLRKRWLYKNTLVKIDHAKV 417
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 450 KHKRFLQAIHQ---LRSYMER 470
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 818 KHKRFLQAIHQ---LRSYMER 441
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 510 LETKLETLGLSIHALPGLSIQ 532
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 871 IHHQLSDISRELISLAEILKGSV 893
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
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DR INTERPRO: IPR001622; -
 KW Ionic channel.
 SQ SEQUENCE 424 AA; 47759 MW; ED874ECAD7F8464D CRC64;

Query Match 30.0%; Score 886.5; DB 11; Length 424;
 Best Local Similarity 44.8%; Pred. No. 3,9e-55;
 Matches 189; Conservative 72; Mismatches 148; Indels 13; Gaps 4;

OY 121 LGHRALEFEKRRKLSYALIFGFIYVYVETELSGVADKASYSALCLISSTII 180
 DB 12 LRRRRKLEOEKRVAGWALVLAAGTIGLVLHAEMLFQCKWVLYLLVCLITISTAF 71
 OY 181 LGLIIVYHAREIQLEFVNDGADMRIMTYERIFFCLEILVCAIHPIR-GNTETWTA 239
 DB 72 LCLLIYVHAKVEQLFMTDNGLRDWRVRLTRROYAOLLELLVCGHVEPLRSPHCTLAG 131
 OY 240 RLAFSAPSTTADVDIILSIPWFLVLYLVARVMLHSLKLFUDASSRSIGALKINENTR 299
 DB 132 EATDSQAMPCEFLGEGEALLSLAMLRLLVPRVALLSGVLLNASYSIGALNQVRRHM 191
 OY 300 FVAKLTMTICPGVLVLFESILMIATVYRACERYHDQDYSNPLGAMLLSTIFLSI 359
 DB 192 FVAKLYMTHPGRLLEGLTIGLMTTAVLSVAER--QAVNATGHLTDTLPTFLTI 249
 OY 360 GYGDVYPTTCGKGVCLLTGIMAGCTALVAVVARRKLELTKAEKRVHNFMDTOLTKRY 419
 DB 250 GYGDVYPTGKGVCLLTGIMAGCTALVAVVARRKLELTKAEKRVHNFMDIHYAKEM 309
 OY 420 KNAANVLRETMLYKNTKLVKKIDHAKVRKHOKRFLQAHOLRSYKOEKRLNDQNTL 479
 DB 310 KESARALQEAAMYYKHT---RRKDSRAARRHOKKMAAHTFRVYRLKHKLEQVNSM 366
 OY 480 VDLAKTONIMTMSLDNERSDEPERIVTLETLETLGSHALPGLSITRQODRF 539
 DB 367 VDLSKMHMLTCDQLGLSHSLALEKRIGHLARKLD-----ALTELLSALDOOPPEP 419
 OY 540 IE 541
 DB 420 IQ 421

RESULT 14
 ID 015554 PRELIMINARY; PRT: 427 AA.
 AC 015554;
 DT 01-JAN-1998 (Tremblrel. 05, Created)
 DT 01-JAN-1998 (Tremblrel. 05, last sequence update)
 DT 01-JUN-2000 (Tremblrel. 14, last annotation update)
 DE INTERMEDIATE CONDUCTANCE CALCIUM-ACTIVATED POTASSIUM CHANNEL (PUTATIVE
 DE EXTHROCYTE INTERMEDIATE CONDUCTANCE CALCIUM-ACTIVATED POTASSIUM
 DE GARDOS CHANNEL).
 GN HKCA4 OR HSK4 OR IK1.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxId=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Gnanashai S., Coleman M., Wu A.C.-L., Gargus J.J., Gultman G.A.,
 RL Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Tissue-Placenta;
 RX MEDLINE=97454570;
 RA Joiner W.J., Wang L.Y., Tang M.D., Kaczmarek L.K.;
 RL Proc. Natl. Acad. Sci. U.S.A. 94:11013-11018(1997).
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Tissue-Placenta;
 RC Joiner W.J., Wang L.-Y., Tang M.D., Kaczmarek L.K.;
 RL Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.

RN [4]
 RP SEQUENCE FROM N.A.
 RC Tissue-Lymph Node;
 RX MEDLINE=98070459; PubMed=9407042;
 RA Logsdon N.J., Kang J., Togo J.A., Christian E.P., Aiyar J.;
 RT "A novel gene, hKCA4, encodes the calcium-activated potassium channel
 in human T lymphocytes." J. Biol. Chem. 272:32723-32726(1997).
 RN [5]
 RP SEQUENCE FROM N.A.
 RA Ishii T.M., Silvia C., Hirschberg B., Bond C.T., Adelman J.P.,
 RA Mayle J.;
 RL Proc. Natl. Acad. Sci. U.S.A. 0:0-0(1997).
 RN [6]
 RP SEQUENCE OF 227-367 FROM N.A.
 RA Golding S., Culliford S.J., Ellory J.C.;
 RT "hK1 (putative Gardos channel) PCR product amplified from the K562
 human erythroleukemic cell line." J.
 RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF033021; AAC36804.1; -
 DR EMBL: AF000972; AAB82739.1; -
 DR EMBL: AF022797; AAC51913.1; -
 DR EMBL: AF023150; AAC23541.1; -
 DR EMBL: AF033403; AAC35281.1; -
 DR INTERPRO: IPR001622; -
 KW Ionic channel.
 SQ SEQUENCE 427 AA; 47695 MW; 23F9AF6609B410P CRC64;

Query Match 29.8%; Score 880.5; DB 4; Length 427;
 Best Local Similarity 43.4%; Pred. No. 1e-54;
 Matches 188; Conservative 71; Mismatches 131; Indels 43; Gaps 7;

OY 121 LGHRALEFEKRRKLSYALIFGFIYVYVETELSGVADKASYSALCLISSTII 180
 DB 12 LRRRRKLEOEKRVAGWALVLAAGTIGLVLHAEMLFQCKWVLYLLVCLITISTAF 71
 OY 181 LGLIIVYHAREIQLEFVNDGADMRIMTYERIFFCLEILVCAIHPIR-GNTETWTA 239
 DB 72 LCLLIYVHAKVEQLFMTDNGLRDWRVRLTRROYAOLLELLVCGHVEPLRSPHCTLAG 131
 OY 240 RLAFSAPSTTADVDIILSIPWFLVLYLVARVMLHSLKLFUDASSRSIGALKINENTR 299
 DB 132 EATDSQAMPCEFLGEGEALLSLAMLRLLVPRVALLSGVLLNASYSIGALNQVRRHM 191
 OY 300 FVAKLTMTICPGVLVLFESILMIATVYRACERYHDQDYSNPLGAMLLSTIFLSI 359
 DB 192 FVAKLYMTHPGRLLEGLTIGLMTTAVLSVAER--QAVNATGHLTDTLPTFLTI 249
 OY 360 GYGDVYPTTCGKGVCLLTGIMAGCTALVAVVARRKLELTKAEKRVHNFMDTOLTKRY 419
 DB 250 GYGDVYPTGKGVCLLTGIMAGCTALVAVVARRKLELTKAEKRVHNFMDIHYAKEM 309
 OY 420 KNAANVLRETMLYKNTKLVKKIDHAKVRKHOKRFLQAHOLRSYKOEKRLNDQNTL 479
 DB 310 KESARALQEAAMYYKHT---RRKDSRAARRHOKKMAAHTFRVYRLKHKLEQVNSM 366
 OY 480 VDLAKTONIMTMSLDNERSDEPERIVTLETLETLGSHALPGLSITRQODRF 539
 DB 367 VDLSKMHMLTCDQLGLSHSLALEKRIGHLARKLD-----ALTELLSALDOOPPEP 419
 OY 540 IE 541
 DB 420 IQ 421

RESULT 15
 ID 09WAC7 PRELIMINARY; PRT: 196 AA.
 AC 09WAC7;
 DT 01-MAY-2000 (Tremblrel. 13, Created)
 DT 01-MAY-2000 (Tremblrel. 13, last sequence update)
 DT 01-MAY-2000 (Tremblrel. 13, last annotation update)

DE CG4179 PROTEIN.

GN CG4179.

OS Drosophila melanogaster (Fruit fly).

OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

OC Ephydroidea; Drosophilidae; Drosophila.

OX NCBI_TaxID:7227;

RM [1]

RP SEQUENCE FROM N.A.

RC STRAIN-BERKELEY;

RA MEDLINE-20196006; PubMed-10731132;

RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,

RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,

RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,

RA Brandon R.C., Rogers J.H.C., Blazer R.G., Champe M., Pfeiffer B.D.,

RA Abail J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,

RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,

RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,

RA Borokova D., Botchan M.R., Bouck J., Brokstein P., Brottler P.,

RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,

RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,

RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,

RA Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,

RA Glodex A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,

RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,

RA Hostlin D., Houston K.A., Howland T.J., Wei M.-H., Idegawa C.,

RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,

RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,

RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,

RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,

RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,

RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacle J.M.,

RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,

RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,

RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,

RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,

RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,

RA Wang Z.-Y., Wasserman D.A., Weinstock G.M., Weissenbach J.,

RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,

RA Ye J., Yen K.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,

RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,

RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;

RT "The genome sequence of Drosophila melanogaster.";

RT Science 287:2185-2195(2000).

RT EMBL: AEO03434; AAF46029.1; .

DR EMBL: AEO03434; AAF46029.1; .

DR FLTBASE: FBgn029760; CG4179.

SQ SEQUENCE 196 AA; 22275 MW; 6E4BFF91CB7C3C9 CRC64;

Query Match

Best Local Similarity 72.3%; Score 717; DB 5; Length 196;

Matches 142; Conservative 19; Mismatches 32; Indels 2; Gaps 2;

Search completed: May 14, 2001, 20:39:42
Job time: 6741 sec

Tue May 15 08:41:28 2001

us-09-254-590-19.rspt

Page 10

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OK protein - protein search, using sw model

Run on: May 14, 2001, 18:48:35 ; Search time 31.16 Seconds
(without alignments)
636.519 Million cell updates/sec

Title: US-09-254-590-19

Perfect score: 2954
Sequence: 1 MSSCRNGSVWRPLSNLSAS.....SSRRRRSSTAPPTSSSS 579

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 93435 seqs, 3425486 residues

Total number of hits satisfying chosen parameters: 93435

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_39:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Query Length	DB ID	Description
1	669	22.6	471	1	YX11_CAEEL
2	189	6.4	695	1	CI04_HUMAN
3	169.5	5.7	872	1	CI03_HUMAN
4	166.5	5.6	924	1	CI03_DROME
5	149.5	5.1	757	1	CI04_HUMAN
6	146.5	5.0	769	1	CI04_MOUSE
7	144.5	4.9	889	1	CI04_MOUSE
8	141.5	4.8	1264	1	CI04_MOUSE
9	140.5	4.8	498	1	CI04_MOUSE
10	138.5	4.7	476	1	EVX2_HUMAN
11	137.5	4.7	475	1	EVX2_MOUSE
12	135	4.6	490	1	CI04_MOUSE
13	134.5	4.6	533	1	CI04_MOUSE
14	134.5	4.6	1262	1	CI04_MOUSE
15	134	4.5	582	1	CI04_MOUSE
16	133.5	4.5	663	1	DUS8_HUMAN
17	132.5	4.5	391	1	HME1_HUMAN
18	132	4.5	625	1	CI04_MOUSE
19	132	4.5	2248	1	CI04_MOUSE
20	129	4.4	604	1	CI04_MOUSE
21	128.5	4.4	671	1	HME1_HUMAN
22	125.5	4.2	440	1	FXGA_CHICK
23	125.5	4.2	676	1	CI01_HUMAN
24	125.5	4.2	853	1	CI04_MOUSE
25	125	4.2	433	1	HXB3_MOUSE
26	125	4.2	549	1	CI04_MOUSE
27	122.5	4.1	497	1	BRN1_MOUSE
28	121.5	4.1	638	1	CI04_MOUSE
29	120.5	4.1	854	1	CI04_MOUSE
30	120	4.1	370	1	MAF2_MOUSE
31	120	4.1	829	1	EVX2_MOUSE
32	118.5	4.0	495	1	BRN1_MOUSE
33	118.5	4.0	500	1	BRN1_HUMAN

34	118	4.0	1067	1	SGG_DROME	P18431 drosophila
35	117	4.0	367	1	BPT3_MESAU	O09029 mesocricetu
36	117	4.0	508	1	CI04_MOUSE	P32027 drosophila
37	116.5	3.9	431	1	HXB3_HUMAN	P14651 homo sapien
38	116.5	3.9	1407	1	CI04_MOUSE	O03100 dictyostell
39	116	3.9	369	1	MAF2_MOUSE	P54844 rattus norv
40	116	3.9	979	1	REF1_HUMAN	P22670 homo sapien
41	115.5	3.9	523	1	CI04_MOUSE	P22001 homo sapien
42	115.5	3.9	919	1	ANDR_HUMAN	P10275 homo sapien
43	115	3.9	165	1	GRP1_ORYSA	P25074 oryza sativ
44	115	3.9	206	1	TWST_MOUSE	P26687 mus musculu
45	115	3.9	410	1	BRN3_HUMAN	Q12837 homo sapien

ALIGNMENTS

RESULT 1	YX11_CAEEL	STANDARD;	PRT; 471 AA.
AC	Q11122;		
DT	01-NOV-1997 (Rel. 35, Created)		
DT	01-NOV-1997 (Rel. 35, Last sequence update)		
DT	01-NOV-1997 (Rel. 35, Last annotation update)		
DE	HYPOTHETICAL 54.3 KDA PROTEIN C03F11.1 IN CHROMOSOME X.		
CN	C03F11.1		
OS	Caenorhabditis elegans.		
OC	Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditidae; Rhabditidae;		
OC	Rhabditidae; Pelodierinae; Caenorhabditis.		
OX	NCBI_TaxID=6239;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=BRISTOL NZ;		
RA	Bentley D.;		
RL	Submitted (01-1995) to the EMBL/GenBank/DBJ databases.		
CC	-i- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).		
CC	-i- This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL Outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).		
CC	EMBL: U39744; AAA80439.1; .		
DR	WormPep; C03F11.1; CE03913.		
KW	Hypothetical protein; Transmembrane.		
FT	TRANSMEM 78 98		POTENTIAL.
FT	TRANSMEM 121 141		POTENTIAL.
FT	TRANSMEM 157 177		POTENTIAL.
FT	TRANSMEM 263 283		POTENTIAL.
FT	TRANSMEM 328 348		POTENTIAL.
SQ	SEQUENCE 471 AA; 54338 MW; C38F384125A3A830 CRC64;		
Query Match	22.6%; Score 669; DB 1; Length 471;		
Best local Similarity	34.3%; Pred. No. 1e-34;		
Matches 158; Conservative 92; Mismatches 136; Indels 74; Gaps 13;			
QY	96 GGGSGHSSSSGSSKKKNQNG-----YKIGRRALPEKKRSLDYALFGMF 144		
DB	30 GSVSHNTSS--AFQRNRSRYGPIIDSTVAVKQYRVSER--LTNRVTRTBSLYALF 84		
QY	145 GIVVAVIETELS--WGAVDKASLYSLAKCLISITILLGLITYHAREQLPMVNG 201		
DB	85 GVIILAVESITAEKRYGVSKTHWISQSLVGTCTIALLYHILYHLNDVLELVDCG 144		
QY	202 ADDRMIAVTEREFCEIIVCAIHPIPGNYFFWTFARLAFSAVS-----248		
DB	145 ADDRMVYVTERIYQICIEFCICGCPPLSGSKMT-----FLEPLHMDGSEERTVQ 199		
QY	249 TTAD--VDIILSPWELRLIARVWLISKLFPTDASRSIGLANKINNRFRVWKLM 306		

Db 200 TRNDVPPDVLLSCFMLCSYLFARFVWLSKQFQDASRTTAAANLRQVNFSEVTKTSL 259
 Oy 307 TJCPTGVLLVESISLWIAATVTRACERY-----HDQDVTNPLGAMWLTSTFTSTCY 361
 Db 260 DQDQVPLFTFTFTFTFIFWMSWMEVOCERYGSGKNPOSTLYSN---SLMEIATFPLNGY 316
 Oy 362 GDMVNTVCGKVCCLLTGIMGAGCTALVAVARVKELTKAKKHHNFMMDTOLTRVYN 421
 Db 317 GDIVPQTAGCFIAIFGVGVAVISSILAVISNLTLSGQGRVNNFMPTDSKLAREHKE 376
 Oy 422 AAANYLRETLITKNTKLVKKID--HAKVRKHOKFLQAIHQLRSVYKQEQKINDOANTL 479
 Db 377 AAARVLQHTWHIH---KCLQSGDGGNRLRYORFKFLAIHFRSVKSEMR----- 425
 Oy 480 VDLAKQINWYDMISDLNERSDEFEKRIYV-LETKLETTI 518
 Db 426 -----FSENNQNNPQRTLVYDMHTMSQRL 452

RESULT 2

C104_HUMAN STANDARD: PRT: 695 AA.

AC P56696; 096025;
 DT 15-JUL-1999 (Rel. 38, Created)
 DT 15-JUL-1999 (Rel. 38, Last sequence update)
 DT 01-OCT-2000 (Rel. 40, Last annotation update)
 DE VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN KQT-LIKE 4.
 GN KCNQ4.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A., AND VARIANT DFN2 SER-285.
 RX MEDLINE=99148276; PubMed=10025409;
 RA Kubisch C., Schroeder B.C., Friedrich T., Luetjohann B.,
 RA El-Amraoui A., Marlin S., Pelic C., Jentsch T.J.;
 RT "KCNQ4, a novel potassium channel expressed in sensory outer hair
 RT cells, is mutated in dominant deafness";
 RL Cell 96:437-446(1999).
 RN [2]
 RP VARIANTS DFN2 SER-276; CYS-285 AND SER-321.
 RX MEDLINE=9929248; PubMed=10369879;
 RA Coucke P.J., Van Hauwe P., Kelley P.M., Kunst H., Schattman I.,
 RA Van Velzen D., Meyers J., Einsink R.J., Verstreken M., Declau F.,
 RA Marres H., Kascunly K., Bhasin S., McGuilt W.T., Smith R.J.H.,
 RA Cremers C.W.R.J., Van de Heyning P., Willems P.J., Smith S.D.,
 RA Van Camp G.;

RT "Mutations in the KCNQ4 gene are responsible for autosomal dominant
 RT deafness in four DFN2 families";
 RL Hum. Mol. Genet. 8:1321-1328(1999).
 CC -1- FUNCTION: MAY BE RESPONSIBLE FOR POTASSIUM IONS AFTER STIMULATION
 CC OF THE HAIR CELL.
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
 CC -1- TISSUE SPECIFICITY: EXPRESSED IN THE OUTER, BUT NOT THE INNER,
 CC SENSOR HAIR CELLS OF THE COCHLEA.
 CC -1- DOMAIN: THE SEGMENT S4 IS PROBABLY THE VOLTAGE-SENSOR AND IS
 CC CHARACTERIZED BY A SERIES OF POSITIVELY CHARGED AMINO ACIDS AT
 CC EVERY THIRD POSITION (BY SIMILARITY).
 CC -1- DISEASE: DEFECTS IN KCNQ4 ARE A CAUSE OF AUTOSOMAL DOMINANT
 CC NONSYNDROMIC SENSORIENURAL DEAFNESS TYPE 2 (DFN2).
 CC -1- SIMILARITY: THIS CHANNEL PROTEIN BELONGS TO THE DELAYED RECTIFIER
 CC CLASS. KQT SUBFAMILY.
 CC -----
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 CC or send an email to license@isb-sib.ch).

DR EMBL: AF105202; AAD14680.1; -;
 DR EMBL: AF105216; AAD14681.1; -;
 DR EMBL: AF105203; AAD14681.1; JOINED.
 DR EMBL: AF105204; AAD14681.1; JOINED.
 DR EMBL: AF105205; AAD14681.1; JOINED.
 DR EMBL: AF105206; AAD14681.1; JOINED.
 DR EMBL: AF105207; AAD14681.1; JOINED.
 DR EMBL: AF105208; AAD14681.1; JOINED.
 DR EMBL: AF105209; AAD14681.1; JOINED.
 DR EMBL: AF105210; AAD14681.1; JOINED.
 DR EMBL: AF105211; AAD14681.1; JOINED.
 DR EMBL: AF105212; AAD14681.1; JOINED.
 DR EMBL: AF105213; AAD14681.1; JOINED.
 DR EMBL: AF105214; AAD14681.1; JOINED.
 DR EMBL: AF105215; AAD14681.1; JOINED.
 DR EMBL: AF105215; AAD14681.1; JOINED.
 DR MIM: 603537; -;
 DR MIM: 600101; -;
 DR InterPro: IPR000636; -;
 DR InterPro: IPR003091; -;
 DR Pfam: PF00520; Ion.trans. 1.
 DR PRINTS: PR00169; KCHANNEL.
 KW Multigene family; Transmembrane; Ion transport; Voltage-gated channel;
 KW Ionic channel; Disease mutation; Deafness.
 FT TRANSMEM 45 65
 FT TRANSMEM 98 118
 FT TRANSMEM 132 152
 FT TRANSMEM 173 193
 FT TRANSMEM 238 258
 FT TRANSMEM 298 318
 FT TRANSMEM 276 276
 FT VARIANT 276 276
 FT VARIANT 285 285
 FT VARIANT 285 285
 FT VARIANT 285 285
 FT VARIANT 321 321
 FT SEQUENCE 695 AA; 77091 MM; A58737BD45E1A3A CRC64;
 /FTID=VAR.008726.
 G -> C (IN DFN2); LOSS OF POTASSIUM
 SELECTIVITY OF THE PORE).
 /FTID=VAR.008727.
 G -> S (IN DFN2).
 /FTID=VAR.001547.
 G -> S (IN DFN2).
 /FTID=VAR.008728.

Query Match 6.4%; Score 189; DB 1; Length 695;
 Best Local Similarity 22.4%; Pred. No. 0.00011;
 Matches 101; Conservative 58; Mismatches 139; Indels 152; Gaps 22;
 Oy 36 PPAVSG-GCGGASPSAAAAAASSAPETIVSKPEHNNSNLTALYGTGGGS----- 89
 Db 5 PPRRLGPPPDPAARAEVLAVALAVOEGE-----AGGSGSPRLG 46
 Oy 90 -----TGGGGGGGGSGHSSGTSKKKNQIKYKIGHRRALFEKRLSDYALITG 142
 Db 47 LLSGPPPEAPPLPGGSGSGSACGGRSS-----AAHKRYRLQW----- 86
 Oy 143 MGVIVVETETELSGAVDKASLYSLAKCLT--SLSTIIILGLIIVHAREIQLEFWVN 200
 Db 87 ----YVNVLEBRGMAYVHVFELLYSCVLVSTI-----QEHDL----- 127
 Oy 201 GADDMKIAMTIRIFELCEIIV-----CAHPIDQNTFTTARLASVAPSTTAD 253
 Db 128 -ANECLILEFVMIVVEGLLEYIVKWSAGCCRRY-----GMOGRFRFRKPCV-- 176
 Oy 254 VDIILISPEFLRLILARVLL-----HSKLTPTDSSRS---IGALNKINFTPRVYKTL 306
 Db 177 IDRTV-----FVASVAVIAAGQGNITATSLRSKRFQIILRWYRDRGRGTRKLL 227
 Oy 307 TJCPTGVLLVES--ISLW-----ITAAWTYRACERYHDQDVTNPLGAMWLTSTFT 356
 Db 228 ----GSVYVASKELITAWYIGELVILFASFLVLEK--DANSDFSSYADSLMGCTITL 281
 Oy 357 LSTIGGVWVPTTYCGK-----GVCLL-----TGIMGAGCTALVAVARVKELTKAKK 404
 Db 282 TTIGVGDTPTPTWTVGRVLAAGFALLGISFPALPAGTIGSG-----FALKVQEDHOK 333

QY 405 HVHFMMDTOLTKRVKNAANVLRTELWLY 434
 DB 334 HFEKRRM-----PAANLLOAMRLY 353

RESULT 3
 CIO3_HUMAN STANDARD; PRT; 872 AA.
 AC 043525;
 DT 15-JUL-1999 (Rel. 38, Created)
 DT 01-JUL-1999 (Rel. 38, Last sequence update)
 DT 01-OCT-2000 (Rel. 40, Last annotation update)
 DE VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN KQT-LIKE 3.
 GN KQT3.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 OX NCBI_Taxid=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=9087323; PubMed=9872318;
 RA Schroeder B.C., Kudisch C., Stein V., Jentsch T.J.;
 RT "Moderate loss of function of cyclic-AMP-modulated KCNQ3 K+
 channels causes epilepsy";
 RL Nature 396:687-690(1998).
 RN [2]
 RP SEQUENCE OF 48-872 FROM N.A. AND VARIANT EBN2 VAL-310.
 RX MEDLINE=98085869; PubMed=9425900;
 RA Charlier C., Singh N.A., Ryan S.G., Lewis T.B., Reus B.E., Leach R.J.,
 RA Leppert M.;
 RT "A pore mutation in a novel KQT-like potassium channel gene in an
 idiopathic epilepsy family";
 RL Nat. Genet. 18:53-55(1998).
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN
 CC -1- DOMAIN: THE SEGMENT S4 IS PROBABLY THE VOLTAGE-SENSOR AND IS
 CC CHARACTERIZED BY A SERIES OF POSITIVELY CHARGED AMINO ACIDS AT
 CC EVERY THIRD POSITION (BY SIMILARITY).
 CC -1- DISEASE: DEFECTS IN KCNQ3 ARE THE CAUSE OF BENIGN FAMILIAL
 CC NEONATAL CONVULSIONS TYPE 2 (BNCE2); ALSO KNOWN AS EPILEPSY,
 CC BENIGN NEONATAL TYPE 2 (EBN2) BNCE2 IS AN AUTOSOMAL-DOMINANT
 CC DISEASE.
 CC -1- SIMILARITY: THIS CHANNEL PROTEIN BELONGS TO THE DELAYED RECTIFIER
 CC CLASS. KQT SUBFAMILY.
 CC -1- SWISS-PROT entry is copyright. It is produced through a collaboration
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 CC
 DR EMBL: AF071491; AAC96101.1; -
 DR EMBL: AF071478; AAC96101.1; JOINED.
 DR EMBL: AF071479; AAC96101.1; JOINED.
 DR EMBL: AF071480; AAC96101.1; JOINED.
 DR EMBL: AF071481; AAC96101.1; JOINED.
 DR EMBL: AF071482; AAC96101.1; JOINED.
 DR EMBL: AF071483; AAC96101.1; JOINED.
 DR EMBL: AF071484; AAC96101.1; JOINED.
 DR EMBL: AF071485; AAC96101.1; JOINED.
 DR EMBL: AF071486; AAC96101.1; JOINED.
 DR EMBL: AF071487; AAC96101.1; JOINED.
 DR EMBL: AF071488; AAC96101.1; JOINED.
 DR EMBL: AF071489; AAC96101.1; JOINED.
 DR EMBL: AF071490; AAC96101.1; JOINED.
 DR EMBL: AF033347; AAB97314.1; -
 DR MIM: 602232; -
 DR MIM: 121201; -
 DR InterPro: IPR000636; -
 DR InterPro: IPR003091; -
 DR Pfam: PF00520; Ion_trans. 1.
 DR PRINTS: PR00169; KCHANNEL.

KM Ionic channel; Transmembrane; Ion transport; Voltage-gated channel;
 KM Multigene family; Disease mutation
 FT TRANSMEM 122 142 POTENTIAL.
 FT TRANSMEM 153 173 POTENTIAL.
 FT TRANSMEM 197 217 POTENTIAL.
 FT TRANSMEM 262 282 POTENTIAL.
 FT TRANSMEM 300 320 POTENTIAL.
 FT TRANSMEM 331 351 POTENTIAL.
 FT VARIANT 310 310 G->V (IN BNCE2).
 FT /FTID=VAR.001546.
 SQ SEQUENCE 872 AA; 96742 MW; BB79C69EB8591A84 CRC64;

Query Match 5.7%; Score 169.5; DB 1; Length 872;
 Best Local Similarity 20.8%; Pred. No. 0.0024;
 Matches 111; Conservative 67; Mismatches 212; Indels 143; Gaps 20.

QY 41 GGGGAGSSSSAAAAAASSAPETIVSKPEHNNNNLLVYGGGSGSGG---GGGG 96
 DB 20 GGGGGAANPAGDADAAA---GDEERKVGALPDVQVTLAL---GAGADKQGTLLSGGG 73
 QY 97 GSGSH-----GSSSGTKSSKKKKNONIGYKLGHRRLFEKRRKLSVALLFGMFGIYV 149
 DB 74 RDEGQRRTPGQIGLLAKTPTLSRPYKRNN---KYRIQT-----LYID 113
 QY 150 VIEFELSMGAVDKASVSLAKCLISLTLLGLIIVYAREIQLFVYDNGADWRIAM 209
 DB 114 ALERPKRMALLHALVFLVYGLCL-----LANLTFFKYE-----TVSGDWILL 159
 QY 210 TYERIFPCLLELY-----CAIHPIGNTFTFTANLAFSTAPSTTADVDITLSPM 262
 DB 160 ETEAFIFEGAEFALRIMAGCCCRK-----GRRGLKFAKRPCLMDIFVLASVPV 212
 QY 263 F-----LRVYLARVM-----LHSLKFTDASSSISGALKINEN 297
 DB 213 VAVNGNGLVATLSRIFQLILMLNDRGGTKLLGSAIC--AKSKELLTAWYIGEL 270
 QY 298 TRFYVKTLLMTICGVYLVFESISMITAAMYVACERHDOODVTSNFGAMWLISITFL 357
 DB 271 T-----LILSFLVLYEKDPEVDQGEKEKEFEETVADALMGLITLA 315
 QY 358 STGYGDMVPTVYCGKVCCLTGINGAGCTALVAVAVARKLELTKAEKHVHFMMDTOLTK 417
 DB 316 TIGYDQKPTKPTWEGRLIATFSLIGSFPAIGLISGLAKVOEOH-----ROKHEK 370
 QY 418 RYKNAANV-----LRETWLYIKNTKIVKIKDKHAKYKROKFLQAIHQ 462
 DB 371 RRRPAAELIOAMRYATNPNRIDIVATWRFYEV---VSFFPKKEQ---LEBASQ 422
 QY 463 RYVKKRQRKLNDO--ANTLVDLAKTONIMYDMSIDLSNRSDEPKRIVTLTK 513
 DB 423 KIGLDVRRLSNRSGNTGKLFPELVN-----DAIESPSKPKPVGIANK 469

RESULT 4
 CIO3_HUMAN STANDARD; PRT; 924 AA.
 AC P17970;
 DT 01-NOV-1990 (Rel. 16, Created)
 DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN SHAB (SHAB11).
 GN SHAB OR SHAB11.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 CC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_Taxid=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=90239553; PubMed=2333511;
 RA Wei A., Covarrubias M., Butler A., Baker K., Pak M., Saikoff L.;
 RT "K+ current diversity is produced by an extended gene family

RT conserved in Drosophila and mouse.":
 RL Science 248:599-603(1990).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=90245668; PubMed=2336395;
 RA Wei A., Covarrubias M., Butler A., Baker K., Pak M., Salkoff L.;
 RT "Shal, Shab, and Shaw: three genes encoding potassium channels in
 Drosophila."
 RL Nucleic Acids Res. 18:2173-2174(1990).
 CC -1- FUNCTION: THIS PROTEIN MEDIATES THE VOLTAGE-DEPENDENT POTASSIUM
 CC ION PERMEABILITY OF EXCITABLE MEMBRANES. ASSUMING OPENED OR CLOSED
 CC CONFORMATIONS IN RESPONSE TO THE VOLTAGE DIFFERENCE ACROSS THE
 CC MEMBRANE, THE PROTEIN FORMS A POTASSIUM-SELECTIVE CHANNEL THROUGH
 CC WHICH K+ IONS MAY PASS IN ACCORDANCE WITH THEIR ELECTROCHEMICAL
 CC GRADIENT.
 CC -1- SUBUNIT: HETEROTETRAMER OF POTASSIUM CHANNEL PROTEINS (PROBABLE).
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
 CC -1- DOMAIN: THE AMINO TERMINUS MAY BE IMPORTANT IN DETERMINING THE
 CC RATE OF INACTIVATION OF THE CHANNEL WHILE THE TAIL MAY PLAY A ROLE
 CC IN MODULATION OF CHANNEL ACTIVITY AND/OR TARGETING OF THE CHANNEL
 CC TO SPECIFIC SUBCELLULAR COMPARTMENTS.
 CC -1- MISCELLANEOUS: THE SEGMENT S4 IS PROBABLY THE VOLTAGE-SENSOR AND
 CC IS CHARACTERIZED BY A SERIES OF POSITIVELY CHARGED AMINO ACIDS AT
 CC EVERY THIRD POSITION.
 CC -1- SIMILARITY: THIS CHANNEL PROTEIN BELONGS TO THE DELAYED RECTIFIER
 CC CLASS. BELONGS TO SHAB POTASSIUM CHANNEL SUBFAMILY.
 CC -----
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 CC -----
 DR EMBL: M32659; AAA2896.1; -
 DR PIR: S15058; S15058.
 DR HSP: P01551; 1ACX.
 DR P1ybaae; FBgn0003583; Shab.
 DR InterPro: IPR000636; -
 DR Pfam: PF00520; Ion_trans; 1.
 DR PRINTS: PR00169; KCHANNEL.
 KW Ionic channel; Transmembrane; Ion transport; Voltage-gated channel;
 KM Glycoprotein; Multigene family; Phosphorylation.
 FT TRANSMEM 436 454 SEGMENT S1.
 FT TRANSMEM 474 495 SEGMENT S2.
 FT TRANSMEM 506 527 SEGMENT S3.
 FT TRANSMEM 536 561 SEGMENT S4.
 FT TRANSMEM 577 598 SEGMENT S5.
 FT TRANSMEM 638 659 SEGMENT S6.
 FT CARBOHYD 245 245 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 429 429 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 530 530 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 749 749 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 756 756 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 885 885 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 888 888 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT MOD_RES 690 690 PHOSPHORYLATION (BY CAPK) (POTENTIAL).
 FT MOD_RES 731 731 PHOSPHORYLATION (BY CAPK) (POTENTIAL).
 FT MOD_RES 796 796 PHOSPHORYLATION (BY CAPK) (POTENTIAL).
 FT SEQUENCE 924 AA; 99698 MW; F4F74205C7020758 CRC64;

Query Match 5.6%; Score 166.5; DB 1; Length 924;
 Best Local Similarity 19.8%; Pred. No. 0.004;
 Matches 143; Conservative 89; Mismatches 222; Indels 269; Gaps 35;

QY 38 ASYGGGAGASSPAAAAAAVSSAPETIVSKPEHH--NSNNLLXTCG--GGSTG 92
 DB 175 AGTGTGTAGSGGGAAGKEY-RYAP-FPVASPTHIPITSQIVGGVGGVGGASSQ 232
 QY 93 GGGGGGGHGGSSGT-----KSSKKKNONIGYKLG--HRRALF 128

Db 233 SISGVPVPHSQSNPTGALQRTSHRMSSIPPEPFMAQSKAVNSINVGVRHEVLM 292
 QY 129 EKKRL-----SDA----- 138
 Db 293 RULERLPHTRLGRIGECTTHEAIVELCDYSLADNEYFDRHRPKSFSSILNFRTKLHI 352
 QY 139 -----LIFG-----MEGVVVIET-----ELSMG 158
 Db 353 VDEMCLVAFGDDEYMGVDELYLSCQHKYHQKKNENHEMKREASLSGQREEPFGG 412
 QY 159 AVDKASLT-----SLAKCLISLSTI-ILGLIVYHAREIDFWNDGA--DDW 205
 Db 413 KSEVQKLMLEKRPNTSFAARVAVISLFLSTIALTLNLTLPOLQIHIDNGTPODNP 472
 QY 206 RIAMTERIFETCLEILVCAIHPIPGNYTFWTARLAFSAPST-----TVADVIILS 259
 Db 473 QLAM-----VEAVCIT-----WPLEYILRSSSPDKMFKGGLNIIDLAI 515
 QY 260 IMFPLRYL-----LAWMLHSKLFSDASSSIGALNKI 294
 Db 516 LPETVSLELETAKNATDQFQDVRVVRIRIRILRYLKL-----ARSTGLSL 566
 QY 295 NNTREYVAKTLMTCGTVLLVFSISLIIAATVACERYHDOQVTSNFG--AMWL 351
 Db 567 GTLRNSYKEL-----GLIMFLAMGVLIFFSLAY-----FAEKDEKDFVSEAFMW 616
 QY 352 ISIFLSIGYGDVNPVTCGKGVCLLGGAGCAGTALVAVANKLELTKAEKHYHNFMM 411
 Db 617 AGIMTIVGSGDICTPALGK-----VGYVCCICGVLLVAPLPII--VNN-- 662
 QY 412 DTQLTKRYKAAANVIRETWILYNNKLYKKIDHAKVKKHOKFLQIHQLRSVMEQRK 471
 Db 663 -----AEFYKN--QMKRE-----KALKRRALDRAK-----REGSIVSFHHI-NLKDAVAK 705
 QY 472 LNDQANTVLAKTONIMYDMISDLNRSDEPKRIVTLEKLETLGSHALPGLISQT 531
 Db 706 SMDLIDIVDTGQKQNVVHPK-----GKQSTPNIGKQL--DVQSGAPG--HN 749
 QY 532 IRQQQRDFIDQMES-----YDKHYVYNAERSRSSRRSS--STAPPTS 575
 Db 750 LSQDNGSTGSGTGRNPATGTGCKYKVD-HVA-NLNSNLNHRGSSSQDQAVPPS 807
 QY 576 SES 578
 Db 808 FDN 810

RESULT 5
 CTRF_HUMAN STANDARD; PRT; 757 AA.
 AC Q14003;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 01-OCT-2000 (Rel. 40, Last annotation update)
 DE VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN KV3.3 (KSH1IID).
 GN KCNC3.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 OX NCBI_Taxid=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=lens epithelium;
 RX MEDLINE=20179629; PubMed=10712820;
 RA Rae J.L., Shepard A.R.;
 RT "KV3.3 potassium channels in lens epithelium and corneal
 RL endothelium."
 RP Exp. Eye Res. 70:339-348(2000).
 RN [2]
 SEQUENCE OF 291-651 FROM N.A.
 RA Lee J.E., Garbutt J.H., Phillips K.L., Roses A.D.;
 RT "A human chromosome 19 Shaw type potassium channel gene.";

RL Submitted (JAN1992) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: THIS PROTEIN MEDIATES THE VOLTAGE-DEPENDENT POTASSIUM
 CC ION PERMEABILITY OF EXCITABLE MEMBRANES. ASSUMING OPENED OR CLOSED
 CC CONFORMATION IN RESPONSE TO THE VOLTAGE DIFFERENCE ACROSS THE
 CC MEMBRANE, THE PROTEIN FORMS A POTASSIUM-SELECTIVE CHANNEL THROUGH
 CC WHICH K+ IONS MAY PASS IN ACCORDANCE WITH THEIR ELECTROCHEMICAL
 CC GRADIENT.
 CC -1- SUBUNIT: THE VOLTAGE-DEPENDENT POTASSIUM CHANNEL IS A
 CC HETEROTETRAMER OF POTASSIUM CHANNEL PROTEINS (PROBABLE).
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
 CC -1- DOMAIN: THE SEGMENT S4 IS PROBABLY THE VOLTAGE-SENSOR AND IS
 CC CHARACTERIZED BY A SERIES OF POSITIVELY CHARGED AMINO ACIDS AT
 CC EVERY THIRD POSITION.
 CC -1- DOMAIN: THE TAIL MAY BE IMPORTANT IN MODULATION OF CHANNEL
 CC ACTIVITY AND/OR TARGETING OF THE CHANNEL TO SPECIFIC SUBCELLULAR
 CC COMPARTMENTS.
 CC -1- SIMILARITY: THIS CHANNEL PROTEIN BELONGS TO THE DELAYED RECTIFIER
 CC CLASS. BELONGS TO SHAW POTASSIUM CHANNEL SUBFAMILY.
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 CC -----
 CC EMBL: AF055989; AAC24118.1; .
 CC DR EMBL: Z11585; CAA7671.1; .
 CC DR MIM: 176264; .
 CC DR InterPro: IPR000636; .
 CC Pfam: PF00520; Ion_trans; 1.
 CC DR Ionic channel; Transmembrane; Ion transport; Voltage-gated channel;
 CC Glycophorin; Multigene family; Phosphorylation.
 CC KW DOMAIN 1 290
 CC FT TRANSMEM 291 309 SEGMENT S1 (POTENTIAL).
 CC FT DOMAIN 310 350 EXTRACELLULAR (POTENTIAL).
 CC FT TRANSMEM 351 370 SEGMENT S2 (POTENTIAL).
 CC FT DOMAIN 371 379 CYTOPLASMIC (POTENTIAL).
 CC FT TRANSMEM 380 398 SEGMENT S3 (POTENTIAL).
 CC FT DOMAIN 399 411 EXTRACELLULAR (POTENTIAL).
 CC FT TRANSMEM 412 434 SEGMENT S4 (POTENTIAL).
 CC FT DOMAIN 435 447 CYTOPLASMIC (POTENTIAL).
 CC FT TRANSMEM 448 469 SEGMENT S5 (POTENTIAL).
 CC FT DOMAIN 470 517 EXTRACELLULAR (POTENTIAL).
 CC FT TRANSMEM 518 539 SEGMENT S6 (POTENTIAL).
 CC FT DOMAIN 540 757 CYTOPLASMIC (POTENTIAL).
 CC FT DOMAIN 31 38 POLY-PRO.
 CC FT DOMAIN 39 42 POLY-GLN.
 CC FT DOMAIN 81 85 POLY-GLY.
 CC FT DOMAIN 229 234 POLY-GLY.
 CC FT DOMAIN 577 587 POLY-PRO.
 CC FT DOMAIN 596 599 POLY-PRO.
 CC FT DOMAIN 673 673 POLY-ALA.
 CC FT CARBOHYD 320 320 N-LINKED (GLCNAc. . .) (POTENTIAL).
 CC FT CARBOHYD 336 336 N-LINKED (GLCNAc. . .) (POTENTIAL).
 CC FT CARBOHYD 483 483 N-LINKED (GLCNAc. . .) (POTENTIAL).
 CC FT CARBOHYD 483 483 N-LINKED (GLCNAc. . .) (POTENTIAL).
 CC SQ SEQUENCE 757 AA; 80520 MW; 266f6b2bb2ac5a52 CRC64;

Query Match 5.1%; Score 149.5; DB 1; Length 757;
 Best Local Similarity 21.7%; Pred. No. 0.036;
 Matches 97; Conservative 52; Mismatches 149; Indels 149; Gaps 22;

QY 27 MDSEAGPLQPPASVGGGSSPSSAAAAAAYSSAPETIVSRPEHNNSNNLALYGTGG 86
 DB 199 LDFEAP--DPA-----GAANANNAAGHGGDDPA-----GAGG 232
 QY 87 GG-----STGGGGGGGGSSSGTSSKKKNQNGIKGLGHR-----A 126
 DB 233 GGDGAGGELKRLCFQDAGAGGAGGPGAGAGAGT-----WMRMQPRVWA 278
 QY 127 LFEK--RRRLSDVALIFGFGIVVWVETELSGAVDKASLYSLAKCLISLSTIL-- 181

DB 279 LFEDPYSSRAARIYAFASLFT-----LSITTFPLELN 312
 QY 182 LGLIYHAREIQLEWVNGADMDRIAMTERIFFCLEILVCAIHPIPGNTFTATL 241
 DB 313 EGRHISNKTQVQSPICAPENITNVEFETEFVYEGCVW-----FFEEFLMI 367
 QY 242 AF-----SAPSTTADVDDIISIPMFLRLYLARVALLHSKLFPTDASSRSGLAKINF 296
 DB 368 TFCPDKVEFLSSNLT-IDCVAILPFYEVGL-----SGLSKAKVDGLFLVYRF 418
 QY 297 -----NRFVFKTLMTICGTYLVFSLMT-IAATVYRACERY-HDOOD 340
 DB 419 VRLIRIFKLRHFGVLGHTLRSTNEFLLLIFLAGLIFPMYIAERIGADPD 478
 QY 341 VT-SNF-----LGAMWLISITFSLIGDGMVENVYCGK--GYCLTIGMGACTALV 389
 DB 479 ILSNNTTYKNPIGPFWMAY-VMTITLIGDMYKKTMSGLVGCALCALAGVLTAMPVYV 537
 QY 390 V-----AVYARKLELTAKKHV 406
 DB 538 IVNFGMYSLAMAKOKLP-KKKKH 563

RESULT 6
 ID CITE_MOUSE STANDARD; PRT; 769 AA.
 AC Q63959; Q62088;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN KV3.3 (KSH1ID).
 GN KCNC3.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus; Mus.
 OC NCBI_TaxID=10090;
 RN [1]
 RN SEQUENCE FROM N.A. (ISOFORM KV3.3B).
 RX MEDLINE=94132879; PubMed=8301351;
 RA Goldman-Wohl D.S., Chan E., Baird D., Heintz N.;
 RT "KV3.3b: a novel Shaw type potassium channel expressed in terminally
 RT differentiated cerebellar Purkinje cells and deep cerebellar
 RT nuclei";
 RL J. Neurosci. 14:511-522(1994).
 RN [2]
 RN SEQUENCE OF 78-769 FROM N.A. (ISOFORM KV3.3A).
 RP STRAIN=AKR/J;
 RX MEDLINE=92155707; PubMed=1740329;
 RA Chanshah S., Pak M., McPherson J.D., Strong M., Dethlefs B.,
 RA Rasmuth J.J., Salkoff L.A., Gutman G.A., Chandy G.K.;
 RT "Genomic organization, nucleotide sequence, and cellular distribution
 RT of a Shaw-related potassium channel gene, KV3.3, and mapping of KV3.3
 RT and KV3.4 to human chromosomes 19 and 1.";
 RL Genomics 12:190-196(1992).
 CC -1- FUNCTION: THIS PROTEIN MEDIATES THE VOLTAGE-DEPENDENT POTASSIUM
 CC ION PERMEABILITY OF EXCITABLE MEMBRANES. ASSUMING OPENED OR CLOSED
 CC CONFORMATION IN RESPONSE TO THE VOLTAGE DIFFERENCE ACROSS THE
 CC MEMBRANE, THE PROTEIN FORMS A POTASSIUM-SELECTIVE CHANNEL THROUGH
 CC WHICH K+ IONS MAY PASS IN ACCORDANCE WITH THEIR ELECTROCHEMICAL
 CC GRADIENT.
 CC -1- SUBUNIT: THE VOLTAGE-DEPENDENT POTASSIUM CHANNEL IS A
 CC HETEROTETRAMER OF POTASSIUM CHANNEL PROTEINS (PROBABLE).
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
 CC -1- ALTERNATIVE PRODUCTS: THE DIFFERENT FORMS OF KV3.3 ARE PRODUCED
 CC BY ALTERNATIVE SPLICING OF THE SAME GENE.
 CC -1- TISSUE SPECIFICITY: THE KV3.3B ISOFORM IS HIGHLY ENRICHED IN THE
 CC BRAIN, PARTICULARLY IN THE CEREBELLUM, WHERE ITS EXPRESSION IS
 CC CONFINED TO PURKINJE CELLS AND DEEP CEREBELLAR NUCLEI. ISOFORM
 CC KV3.3A IS NOT EXPRESSED IN CEREBELLUM.
 CC -1- DEVELOPMENTAL STAGE: EXPRESSION OF KV3.3B BEGINS IN CEREBELLAR
 CC PURKINJE CELLS BETWEEN POSTNATAL DAY 8 (P8) AND P10 AND CONTINUES
 CC THROUGH ADULTHOOD.

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CC -1- DOMAIN: THE SEGMENT S4 IS PROBABLY THE VOLTAGE-SENSOR AND IS
CC CHARACTERIZED BY A SERIES OF POSITIVELY CHARGED AMINO ACIDS AT
CC EVERY THIRD POSITION.
CC -1- DOMAIN: THE TAIL MAY BE IMPORTANT IN MODULATION OF CHANNEL
CC ACTIVITY AND/OR TARGETING OF THE CHANNEL TO SPECIFIC SUBCELLULAR
CC COMPARTMENTS.
CC -1- SIMILARITY: THIS CHANNEL PROTEIN BELONGS TO THE DELAYED RECTIFIER
CC CLASS. BELONGS TO SHAW POTASSIUM CHANNEL SUBFAMILY.
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CC -----
DR EMBL: S69381; AAC60679.1; -
DR EMBL: X60796; CAA43209.1; -
DR EMBL: X60797; CAA43209.1; JOINED.
DR MGd: M61:96669; Kcnc3.
DR InterPro: IPR000636; -.
DR Pfam: PF00520; Ion_trans; 1.
DR PRINTS: PR00169; KCHANNEL.
KM Glycoprotein; Multigene family; Ion transport; Voltage-gated channel;
KT DOMAIN 1 390
FT TRANSSEM 291 309
FT DOMAIN 310 350
FT TRANSSEM 351 370
FT DOMAIN 371 379
FT TRANSSEM 380 398
FT DOMAIN 399 411
FT TRANSSEM 412 434
FT DOMAIN 435 447
FT TRANSSEM 448 469
FT DOMAIN 470 517
FT TRANSSEM 518 539
FT DOMAIN 540 569
FT DOMAIN 41 44
FT DOMAIN 82 86
FT DOMAIN 229 234
FT DOMAIN 577 587
FT DOMAIN 596 599
FT DOMAIN 659 674
FT CARBOHYD 320 320
FT CARBOHYD 336 336
FT CARBOHYD 483 483
FT VARSPLIC 660 769
FT CONFLICT 256 256
FT CONFLICT 260 266
FT SEQUENCE 769 AA; 82116 MW; BCACD5AB2D6D9EC CRC64;
Query Match 5.08; Score 146.5; DB 1; Length 769;
Best Local Similarity 22.38; Pred. No. 0.0577; Indels 123; Gaps 19;
Matches 87; Conservative 47; Mismatches 134;
OY 83 GTGGGG-----STGGGGGGGGGGSSSGTSSKKKNQNIYKLGHR---125
DB 229 GAGCGGAGGAGGELKRLCFQDAGGAGGILPGAGGAGCT-----WMRMKP 274
OY 126 ---ALFEK--RKRLSDYALFEGFGVYVETLSGALDKASLYSLAKCLISSTII 180
DB 275 RVALFEDPYSSRAKRYVAFASIFEL-----LISITPC 308
OY 181 L---LGLIYVHAREIQLFVWDGADDMRIAMTYERIFICLEILVCAIHIPGNTFTW 237

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DR Pfam: PF00520; Ion_trans; 1.
 DR PRINTS: PR00169; KCHANNEL.
 KW Ionic channel; Transmembrane; Ion transport; Voltage-gated channel;
 FT Glycoprotein; Multigene family; Alternative splicing; Phosphorylation.
 FT DOMAIN 1 291
 FT TRANSMEM 292 310 SEGMENT S1 (BY SIMILARITY).
 FT TRANSMEM 311 351 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 352 371 SEGMENT S2 (BY SIMILARITY).
 FT TRANSMEM 372 380 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 381 399 SEGMENT S3 (BY SIMILARITY).
 FT TRANSMEM 400 412 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 413 435 SEGMENT S4 (BY SIMILARITY).
 FT TRANSMEM 436 448 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 449 470 SEGMENT S5 (BY SIMILARITY).
 FT DOMAIN 471 518 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 519 540 SEGMENT S6 (BY SIMILARITY).
 FT TRANSMEM 541 589 CYTOPLASMIC (POTENTIAL).
 FT CARBOHYD 321 321 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT VARSPLIC 662 679 NDGLYERGDPRNGDPA -> EGARTGVRGGGWSG
 FT VARSPLIC 680 889 MISSING (IN ISOFORM KSHIID.2).
 FT VARSPLIC 889 AA; 94393 MW; 51424C047BAFC367 CRC64;
 SQ SEQUENCE

Query Match 4.98; Score 144.5; DB 1; Length 889;
 Best Local Similarity 22.0%; Pred. No. 0.09;
 Matches 86; Conservative 47; Mismatches 135; Indels 123; Gaps 19;

QY 83 GTGGGG-----STGGGGGGSGHSSGQTKSSKKNNIGYKLGHR-- 125
 DB 230 GAGGGGLDAGGELKRLCFQDAGGAGGAGPGAGGT-----WRRKMP 275
 QY 126 ---ALPER--KKRLSDYALFGMGIVAVITELSMGANDKASLYLAKCLISLSTII 180
 DB 276 RYVAFEDPYSRRARYAPASLFT-----LSITIFC 309
 QY 181 L---LGLIIVHAREIQLEFVWQNDADWRIAMTYRFFTELELVALCAHPGNYFTW 237
 DB 310 LETHGFHHSNKTYTQASPIPGAPENITNVEETPELTYEGCVAV-----FTFEF 364
 QY 238 TARIAR-----SYASTTTADVDTIISIMPLRLTLARWMLHSLFTDASSRISGLN 292
 DB 365 LMRVTECPDKEVLEKSLNT-IDCVALLPEYLEVL-----SGLSKAKKDYLFRL 415
 QY 293 KINF-----NTRFVAKTLMTICPGVLVLFVSISLMI-IAAMTVRACERY-H 336
 DB 416 VVRVRLRLFLKLTFRFVGLVGLHTLRASTNEFLITIFLAGVLIFATMIYVERIGA 475
 QY 337 DQDQVT-SNF-----LGAMWLSTIFSLISYGMVNYTCCK---GYCLLTGIMGAGC 385
 DB 476 DPDDIGSNHTYFKNPIGFWMAV-VTMTTGLIGDMYFKTWISGMLYGAICALAGVLTAM 534
 QY 386 TALVY-----AVYARKLELTKAEKHV 406
 DB 535 PVPYIVNNFCMYSLAMAKOKLP-KKKKHII 564

RESULT 8
 CVA5_RABIT STANDARD; PRT; 1264 AA.
 AC P40144;
 DT 01-FEB-1995 (Rel. 31, Created)
 DT 01-FEB-1995 (Rel. 31, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE ADENYLYL CYCLASE, TYPE V (EC 4.6.1.1) (ATP PYROPHOSPHATE-LYASE)
 DE (ADENYLYL CYCLASE).
 GN ADCT5.
 OS Oryctolagus cuniculus (Rabbit).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
 OC NCBI_TaxID=9986;
 RN [1]
 RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.

RC TISSUE=Myocardium;
 RX MEDLINE=94139935; PubMed=8307190.
 RA Wallach J., Droste M., Kluxen F.-W., Pfeuffer T., Frank R.;
 FT "Molecular cloning and expression of a novel type V adenylyl cyclase
 from rabbit myocardium."
 FT FEBS Lett. 338:257-263(1994).
 RL -1- FUNCTION: THIS A MEMBRANE-BOUND, CA(2+)-INHIBITABLE ADENYLYL
 CYCLASE.
 CC -1- CATALYTIC ACTIVITY: ATP = 3',5'-CYCLIC AMP + PYROPHOSPHATE.
 CC -1- ENZYME REGULATION: INHIBITION BY CA(2+) IN THE SUBMICROMOLAR
 CONCENTRATION RANGE.
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
 CC -1- TISSUE SPECIFICITY: MYOCARDIAL TISSUE.
 CC -1- DOMAIN: COMPOSED OF TWO HOMOLOGOUS DOMAINS.
 CC -1- PTM: THE N-TERMINUS IS BLOCKED.
 CC -1- SIMILARITY: BELONGS TO ADENYLYL CYCLASE CLASS-4/GUANYLYL CYCLASE
 FAMILY.
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 CC EMBL: Z29371; CAB82562.1; -
 DR HSP: P19754; IAKK.
 DR Interpro: IPR001054; -
 DR Pfam: PF00211; guanylate_cyc; 2.
 DR PROSITE: PS00452; GUANYLYLATE_CYCLASES.1; 2.
 DR PROSITE: PS0125; GUANYLYLATE_CYCLASES.2; 2.
 KW Lyase; CAMP synthesis; Transmembrane; Glycoprotein; Duplication.
 FT DOMAIN 1 244
 FT TRANSMEM 245 265 POTENTIAL.
 FT TRANSMEM 271 290 POTENTIAL.
 FT TRANSMEM 301 322 POTENTIAL.
 FT TRANSMEM 331 348 POTENTIAL.
 FT TRANSMEM 351 369 POTENTIAL.
 FT TRANSMEM 377 398 POTENTIAL.
 FT DOMAIN 399 765 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 766 786 POTENTIAL.
 FT TRANSMEM 797 816 POTENTIAL.
 FT TRANSMEM 839 859 POTENTIAL.
 FT DOMAIN 860 912 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 913 933 POTENTIAL.
 FT TRANSMEM 938 958 POTENTIAL.
 FT TRANSMEM 987 1006 POTENTIAL.
 FT DOMAIN 1007 1264 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 1264 145 POLY-ASP.
 FT DOMAIN 145 151 POLY-ASP.
 FT CARBOHYD 873 873 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 890 890 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 975 975 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 1264 AA; 139623 MW; 1787EB42A0C2DF6 CRC64;

Query Match 4.88; Score 141.5; DB 1; Length 1264;
 Best Local Similarity 19.7%; Pred. No. 0.21;
 Matches 108; Conservative 64; Mismatches 209; Indels 167; Gaps 21;

QY 20 SRRLHEMDESKOPIOPASVGGGASPSAAAAAANVSSAPETIVSKREHNNSNL 79
 DB 118 SRRORGACGCGSTRAPGAGCGCG-----SAAAAAAGTEVPSPVELGLEERKGR 173
 QY 80 ALVGTGGGSGTG-GGGGGSGHSSGQTKSSKKNNIGYKLGHRRLFKRRKRLSDYA 138
 DB 174 AVDELEAGANVEGEGEDGSSADSSNGP----- 202
 QY 139 LIFMGIVAVITELSMGANDKASLYLAKCLISLSTIIILGLIIVHAREIQLEFW 198
 DB 203 ---GAV-----LSLGA-----LQIFRS 221

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OY 199 DNGADNRMTATYERIF-----ICLEILVCAHPICGNTTWTARLAFSAPS 248
DB 222 KKEPSD-KLERLQRFREFFLNOSLTMALVAVLY-----MLAFHARP 267
OY 249 TTTADVLIISIPMLRLYLRLARVMLLSKLETFDASSRSIGALKINENTRFVAKTLM1 308
DB 268 P-----LQLEPLAVLAAAGVILVAVLCRRAR-----FHQDMGLA 304
OY 309 CPGVLVFSISLMTAANTVACRCHRDODVTSFGLAMKLSITFLSTGDMVPT 368
DB 305 CALIAYLAVOVVGLLPORPASE-----GIMW--TFEITTYI-TLLP-- 347
OY 365 YCGGVCLLTGAGCTALVAVVARKLELTKAEKHNHNMPTOLTKRVKAAANYLR 428
DB 348 -VRMAVAVLSGV-----LSTLHLATLR-----TNAQ-----DRFL-----KQVLSNV-- 386
OY 429 ETWLTKNTKLVKKIDHAKVRKHQRFLQALHQLBSVKMEQRKINDQANTVDLAKTONI 488
DB 387 ---LIFSCINIVGCTHHPAEVSORAFQETRECTOARLHSHQRENOOERLLSVLPKRV 443
OY 489 MYDMSPLNERSD--FEKRIVLTLETLETLGSHALPGDISQITROQORDFEADOMES 546
DB 444 AMEKADINKAKODMFMFKIYQKHNVSTLEFADIEGFTSLASQCTAOELVMTLWELPAR 503
OY 547 YDKHVTYN 554
DB 504 FDKLAEN 511

RESULT 9
CIRK_DROME STANDARD: PRT: 498 AA.
ID CIRK_DROME
AC P17972: Q9V0U5;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN SHAW (SHAW2).
GN SHAW OR SHAW2 OR CG2822.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90239553; PubMed=233511;
RA Wei A., Covarrubias M., Butler A., Baker K., Pak M., Salkoff L.;
RT "K+ current diversity is produced by an extended gene family
RL conserved in Drosophila and mouse.";
RL Science 248:599-603(1990).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=90245668; PubMed=2336395;
RA Wei A., Covarrubias M., Butler A., Baker K., Pak M., Salkoff L.;
RT "Shal, Shab, and Shaw: three genes encoding potassium channels in
RL Drosophila.";
RL Nucleic Acids Res. 18:2173-2174(1990).
RN [3]
RP SEQUENCE FROM N.A.
RX STRAIN=BERKELEY;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazer V.G., Change M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter A.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Brilli J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borokova D., Botchan M.R., Bouck J., Brokstein P., Brotler P.,
RA Burks K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,

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RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Durbin K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durkin K.J., Evangelista C.C., Ferraz C., Fertler S., Fleischmann W.,
RA Foster C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodex A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Idegawa C.,
RA Jalili M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Kerchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merulov G., Mishina N.V., Mobarry C., Morris J., Moshirefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nussken D.R., Paclebo J.M.,
RA Palazolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner C., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wasserman D.A., Weinstock G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gbbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
RL Science 287:2185-2195(2000).
CC -I- FUNCTION: THIS PROTEIN MEDIATES THE VOLTAGE-DEPENDENT POTASSIUM
CC ION PERMEABILITY OF EXCITABLE MEMBRANES. ASSUMING OPENED OR CLOSED
CC CONFORMATIONS IN RESPONSE TO THE VOLTAGE DIFFERENCE ACROSS THE
CC MEMBRANE, THE PROTEIN FORMS A POTASSIUM-SELECTIVE CHANNEL THROUGH
CC WHICH K+ IONS MAY PASS IN ACCORDANCE WITH THEIR ELECTROCHEMICAL
CC GRADIENT.
CC -I- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -I- MISCELLANEOUS: THE SEGMENT S4 IS PROBABLY THE VOLTAGE-SENSOR AND
CC IS CHARACTERIZED BY A SERIES OF POSITIVELY CHARGED AMINO ACIDS AT
CC EVERY THIRD POSITION.
CC -I- MISCELLANEOUS: THIS CHANNEL PROTEIN BELONGS TO THE DELAYED
CC RECTIFIER CLASS.
CC -I- SIMILARITY: STRONGEST TO MOUSE NGK2.
CC
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DR EMBL: M32661; AAA28897.1; -
DR EMBL: AE003579; AAF51069.1; -
DR PIR: S12748; S12748.
DR FLYBASE: FBgn0003386; Shaw.
DR InterPro: IPR000636; -
DR Pfam: PF00520; Ion.trans.1.
DR PRINTS: PR00169; KCHANNEL.
KW Glycoprotein; Multigene family; Ion transport; Voltage-gated channel;
KW Transmem
FT TRANSMEM 175 193 SEGMENT S1.
FT TRANSMEM 230 252 SEGMENT S2.
FT TRANSMEM 263 284 SEGMENT S3.
FT TRANSMEM 292 313 SEGMENT S4.
FT TRANSMEM 329 350 SEGMENT S5.
FT TRANSMEM 392 413 SEGMENT S6.
FT CARBOHYD 206 206 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 213 213 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 481 481 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ CARBOHYD 498 AA: 56509 MW; 977E3BF2F098E2 CRC64;

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Query Match 4.8%; Score 140.5; DB 1; Length 498;
Best Local Similarity 23.2%; Pred. No. 0.06;

Matches 86; Conservative 48; Mismatches 128; Indels 109; Gaps 18;

QY 144 FGIVVWVETELSMGAYDKAKSL-----ALKCLISLST-----ILLGLIIVH-- 189
 DB 139 FGDEEDYTKGTFISWQEMKRRISLDFEPYSNAKIGVSVFFCISILSFLCKTHPD 198
 QY 190 -----AREIOLEWVNDGADWRI--AMYEKIFLCIEILVCAHPICGNTFTWTRLA 242
 DB 199 MRVPIVRNITY-KTANGSNGMFLDKOTNAHAFFEYIE-CVC-----NMFETELVA 249
 QY 243 ESYAPS-----TTADVDTILSIPIMLRLYL-----IARVALLHSLK 279
 DB 250 FISSPKMEFEIKSSNIIDYIATLSFYIDLVORFASHLEMDIEEFESIRIM-----RL 305
 QY 280 FTDASSRISGALNKINENTREPVKMTLCIPGVLYLPSISLMI--IAANTYRACERY--H 336
 DB 306 F-----KLTIRHSGCLKILITFRASAKETLVLVFLVGLVIFASLYVYARORPN 356
 QY 337 DQDQVTSNFLGAMWLITSTLSIGYGDVNPVTCGKGYCLLTGIMGAGCTALVYAVYARK 396
 DB 357 PHNDPNSIPGLIMWL-VTMTYGYGDMAKTYIGMFVGCALAGVLTALPVPVI--- 412
 QY 397 LEITRAKHAHNPMDTOLTKRYKNAANVLAETLYIKNTKLKIDAKYKHKORFL 456
 DB 413 -----VSNFRM-----YSHTOA-----RAKLPRKRRVYL 437
 QY 457 QAIHQLRSYKM 467
 DB 438 -PVEQPPROPRL 447

RESULT 10
 ID EVX2_HUMAN STANDARD; PRT; 476 AA.
 AC 003828;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-2000 (Rel. 40, Last sequence update)
 DT 01-OCT-2000 (Rel. 40, Last annotation update)
 DE HOMEOBOX EVEN-SKIPPED HOMOLOG PROTEIN 2 (EVX-2).
 GN EVX2.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Birren B., Linton L., Nusbaum C., Lander E.,
 RL Submitted (OCT-2000) to the EMBL/Genbank/DBJ databases.
 RN [2]
 RP SEQUENCE OF 144-300 FROM N.A.
 RX MEDLINE=91257849; PubMed=1675198;
 RA D'Esposito M., Morelli F., Acampora D., Migliaccio E., Simeone A.,
 RA Boncinelli E.;
 RT "EVX2, a human homeobox gene homologous to the even-skipped
 RT segmentation gene, is localized at the 5' end of HOXA locus on
 RT chromosome 2.";
 RL Genomics 10:43-50(1991).
 CC -1- SUBCELLULAR LOCATION: NUCLEAR.
 CC -1- DEVELOPMENTAL STAGE: EXPRESSED DURING EARLY EMBRYOGENESIS AND
 CC NEUROGENESIS IN A BIPHASIC MANNER.
 CC -1- SIMILARITY: BELONGS TO THE EVEN-SKIPPED FAMILY OF HOMEOBOX
 CC PROTEINS.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: AC009336; -; NOT ANNOTATED CDS.
 DR EMBL: M59983; AAA52414.1; -.

DR EMBL: M59982; AAA52414.1; JOINED.
 DR HSSP: P02833; 1SAN.
 DR MIM: 142991; -.
 DR InterPro: IPR001356; -.
 DR Pfam: PF00046; homeobox; 1.
 DR PROSITE: PS00027; HOMEOBOX_1; 1.
 DR PROSITE: PS00071; HOMEOBOX_2; 1.
 KW DNA-binding; developmental protein; Homeobox; Nuclear protein.
 FT DNA BIND 188 247 HOMEOBOX.
 FT DOMAIN 294 301 POLY-ALA.
 FT DOMAIN 304 308 POLY-ALA.
 FT DOMAIN 346 351 POLY-ALA.
 FT DOMAIN 356 370 POLY-ALA.
 FT DOMAIN 373 378 POLY-ALA.
 FT DOMAIN 398 408 POLY-ALA.
 FT DOMAIN 413 434 POLY-GLY.
 SQ SEQUENCE 476 AA; 47799 MW; 6AA99041BA151C3F CRC64;

Query Match 4.7%; Score 138.5; DB 1; Length 476;
 Best Local Similarity 38.5%; Pred. No. 0.1;
 Matches 47; Conservative 11; Mismatches 37; Indels 27; Gaps 6;

QY 11 MRPLSNLSA-----SRNLEHMDSEAOP--IQPPASVGGGCGGSGGSGHSSS 62
 DB 316 IRPLDFFRALSHPSYRPEL--LCSFRHPIGVQAPAAAGNSASASAAAAAASSA 373
 QY 63 -----APEIVVSKP-----EHNNSN-----NLATYGTGGGSGTGGGSGGSGSS 105
 DB 374 AAAGAPPGSGSAPCSCLSCHSSGSAASAAAAAALSGRGGGGGGAGACAGC 433
 QY 106 GT 107
 DB 434 GS 435

RESULT 11
 ID EVX2_MOUSE STANDARD; PRT; 475 AA.
 AC P49749;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE HOMEOBOX EVEN-SKIPPED HOMOLOG PROTEIN 2 (EVX-2).
 GN EVX2 OR EVX-2.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=92249649; PubMed=1349539;
 RA Dush M.K., Martin G.R.;
 RT "Analysis of mouse Evx genes: Evx-1 displays graded expression in the
 RT primitive streak.";
 RL Dev. Biol. 151:273-287(1992).
 CC -1- SUBCELLULAR LOCATION: NUCLEAR.
 CC -1- SIMILARITY: BELONGS TO THE EVEN-SKIPPED FAMILY OF HOMEOBOX
 CC PROTEINS.
 CC -----
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 CC -----
 DR EMBL: S34322; AAB22138.1; -.
 DR EMBL: S34320; AAB22138.1; JOINED.
 DR EMBL: S34321; AAB22138.1; JOINED.
 DR EMBL: M93128; AAA37585.1; -.
 DR HSSP: P04002; 1MFA.

DR MGD: MGI:95462; Evx2.
 DR InterPro: IPR001356;
 DR Pfam: PF00046; homeobox_1.
 DR PRINTS: PR00024; HOMEBOX.1.
 DR PROSITE: PS00027; HOMEBOX_1; 1.
 DR PROSITE: PS00071; HOMEBOX_2; 1.
 KW DNA-binding; Developmental protein; Homeobox; Nuclear protein.
 FT DOMAIN 167 172 POLY-GLY.
 FT DNA_BIND 191 250 HOMEBOX.
 FT DOMAIN 297 304 POLY-ALA.
 FT DOMAIN 307 311 POLY-ALA.
 FT DOMAIN 349 354 POLY-ALA.
 FT DOMAIN 359 373 POLY-ALA.
 FT DOMAIN 376 381 POLY-ALA.
 FT DOMAIN 401 411 POLY-ALA.
 FT DOMAIN 416 429 POLY-GLY.
 SQ SEQUENCE 475 AA; 47902 MW; 2621C6059C76A798 CRC64;

Query Match
 Best Local Similarity 4.78; Score 137.5; DB 1; Length 475;
 Matches 47; Conservative 16; Mismatches 41; Indels 27; Gaps 6;

QY 11 MRPLSNLSA-----SRRLHENDSEAP--LPPASVGGGGGSSPAAAAAAVSS- 62
 DB 319 IRPLDTFRALSHPRSPRL--LCSPRHGLYQAPMAAALNSAAAAAASAAASAA 376
 QY 63 ----APEIVSKP-----EHNSN-----NLALYGGGGGSGGGGGSGHSS 105
 DB 377 AAGAPRPSGSGAPSCSLSCHSSQSSQAAAAAALGSRGGGGGGGAGTAGSDPF 436
 QY 106 GTRSKKKKNON 116
 DB 437 GCSAAAPRSES 447

RESULT 12
 ID CIRC.DROME STANDARD: PRT; 490 AA.
 AC P17971;
 DT 01-NOV-1990 (Rel. 16, Created)
 DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DE 15-JUL-1998 (Rel. 36, Last annotation update)
 OS VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN SHAL2.
 GN SHAL OR SHAL2.
 OS Drosophila melanogaster (fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN 11
 RP SEQUENCE FROM N.A.
 RX MEDLINE=90239553; PubMed=2333511;
 RA Wei A., Covarrubias M., Butler A., Baker K., Pak M., Salkoff L.;
 RT "A current diversity is produced by an extended gene family
 conserved in Drosophila and mouse.";
 RL Science 248:599-603(1990).
 RN 12
 RP SEQUENCE FROM N.A.
 RX MEDLINE=90245668; PubMed=2336395;
 RA Wei A., Covarrubias M., Butler A., Baker K., Pak M., Salkoff L.;
 RT "Shal, Shab, and Shaw: three genes encoding potassium channels in
 Drosophila.";
 RL Nucleic Acids Res. 18:2173-2174(1990).

-1- FUNCTION: THIS PROTEIN MEDIATES THE VOLTAGE-DEPENDENT POTASSIUM
 ION PERMEABILITY OF EXCITABLE MEMBRANES. ASSUMING OPENED OR CLOSED
 CONFORMATIONS IN RESPONSE TO THE VOLTAGE DIFFERENCE ACROSS THE
 MEMBRANE, THE PROTEIN FORMS A POTASSIUM-SELECTIVE CHANNEL THROUGH
 WHICH K+ IONS MAY PASS IN ACCORDANCE WITH THEIR ELECTROCHEMICAL
 GRADIENT. MAY PLAY A ROLE IN THE NERVOUS SYSTEM AND IN THE
 REGULATION OF BEATING FREQUENCY IN PACEMAKER CELLS.
 CC -1- SUBUNIT: HETEROOTETRAMER OF POTASSIUM CHANNEL PROTEINS (PROBABLE).
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.

CC -1- ALTERNATIVE PRODUCTS: SHAL1 AND SHAL2 ARE PRODUCED BY ALTERNATIVE
 SPLICING OF THE SAME GENE.
 CC -1- DOMAIN: THE AMINO TERMINUS MAY BE IMPORTANT IN DETERMINING THE
 RATE OF INACTIVATION OF THE CHANNEL WHILE THE TAIL MAY PLAY A ROLE
 IN MODULATION OF CHANNEL ACTIVITY AND/OR TARGETING OF THE CHANNEL
 TO SPECIFIC SUBCELLULAR COMPARTMENTS.
 CC -1- MISCELLANEOUS: THE SEGMENT S4 IS PROBABLY THE VOLTAGE-SENSOR AND
 IS CHARACTERIZED BY A SERIES OF POSITIVELY CHARGED AMINO ACIDS AT
 EVERY THIRD POSITION.
 CC -1- SIMILARITY: THIS CHANNEL PROTEIN BELONGS TO THE A-TYPE POTASSIUM
 CURRENT CLASS.

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DR EMBL: M32660; AAA28895.1; -
 DR PIR: A35312; A35312.
 DR PIR: S12747; S12747.
 DR FlyBase: FBgn0005564; Shal.
 DR InterPro: IPR000636; -
 DR InterPro: IPR003091; -
 DR Pfam: PF00520; Ion_trans; 1.
 DR PRINTS: PR00169; KCHANNEL.
 KW Ionic channel; Transmembrane; Ion transport; Voltage-gated channel;
 KW Glycoprotein; Multigene family; Alternative splicing.
 FT TRANSMEM 186 204 SEGMENT S1.
 FT TRANSMEM 229 250 SEGMENT S2.
 FT TRANSMEM 261 282 SEGMENT S3.
 FT TRANSMEM 290 308 SEGMENT S4.
 FT TRANSMEM 324 345 SEGMENT S5.
 FT TRANSMEM 385 406 SEGMENT S6.
 FT CARBOHYD 46 46 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 350 350 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 353 353 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 408 408 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 490 AA; 55918 MW; E178E1C89B07DA74 CRC64;

Query Match
 Best Local Similarity 4.64; Score 135; DB 1; Length 490;
 Matches 63; Conservative 38; Mismatches 81; Indels 80; Gaps 11;

QY 213 RIFPCLLELVCAHPIDPQNTPTWTAFLAFSAPS-----TTTADVDIISIPMLRL 266
 DB 226 KIVFCLDTRACYMI-----FTAEYLLRLFAAPDRCKFRVSVMISIIDVAIMPYIGL 277
 QY 267 YLI-----ARVMLLSKFTDASSRSGLMKNINRTFRFKLMTLTCGYLVFESI 319
 DB 278 GIINDNDVSGAFVYLRLFRF-----RLFRSHSGCLRTIGYLKSCASELGFVLESL 331
 QY 320 SLMTIANTVTRACRRHYDDQDT--SNFL--GAMMLISTFSLISGYDMVNTYCK-- 372
 DB 332 AMAIITFAV-----MFAEKNVNGTNTFSIPARVYITVMTTLTGDMVPELTAKIYG 387
 QY 373 GVLGLTGLMGAGCTAAVVAVARKELELKAKEHNPMDDTLTTRKYNAAVAVLEETWL 432
 DB 388 GVCSSLGVL-----VIALPVPYI-----VSNF----- 409
 QY 433 IYKNTKLYKKIDAAKVKRHKQR 454
 DB 410 -----SRIVHONDRDKRAQR 427

RESULT 13
 ZIC2 HUMAN STANDARD: PRT; 533 AA.
 ID ZIC2 HUMAN
 AC Q95409;
 DT 30-MAY-2000 (Rel. 39, Created)

DT 30-MAY-2000 (Rel. 39, last sequence update)
 DT 01-OCT-2000 (Rel. 40, last annotation update)
 DE ZINC FINGER PROTEIN ZIC2 (ZINC FINGER PROTEIN OF THE CEREBELLUM 2).
 GN ZIC2.
 OS Homo sapiens (Human).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 CX NBL_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A. AND VARIANT HPE5 POLY-ALA INSERTION.
 RX MEDLINE=98442655; PubMed=97717172;
 RA Brown S.A., Warburton D., Brown L.Y., Yu C.Y., Roeder E.R.,
 RA Stengel-Rutkowski S., Hennekam R.C., Wenne M.,
 RT "Holoprosencephaly due to mutations in Zic2, a homologue of Drosophila
 RT odd-paired".
 RL Nat. Genet. 20:180-183(1998).
 CC -1- SUBCELLULAR LOCATION: NUCLEAR.
 CC -1- DISEASE: DEFECTS IN ZIC2 ARE A CAUSE OF HOLOPROSENCEPHALY TYPE 5
 CC (HPE5). HPE5 IS A STRUCTURAL ANOMALY OF THE BRAIN.
 CC -1- SIMILARITY: BELONGS TO THE GLI FAMILY OF C2H2-TYPE ZINC-FINGER
 CC PROTEINS.
 CC -----
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 CC -----
 DR EMBL: AF104902; AAC96325.1; -
 DR HSSP: P30129; ADPV.
 DR MIM: 603073; -
 DR InterPro: IPR000822; -
 DR Pfam: PF00096; zf-C2H2; 5.
 DR PROSITE: PS00028; ZINC_FINGER_C2H2_1; 3.
 DR PROSITE: PS50157; ZINC_FINGER_C2H2_2; 4.
 KW Zinc-finger; Metal-binding; DNA-binding; Repeat; Nuclear protein;
 KW disease mutation; Holoprosencephaly.
 FT DOMAIN 20 23 POLY-HIS.
 FT DOMAIN 25 33 POLY-ALA.
 FT DOMAIN 89 97 POLY-ALA.
 FT DOMAIN 227 231 POLY-ALA.
 FT DOMAIN 232 240 POLY-HIS.
 FT DOMAIN 301 416 ZINC_FINGERS.
 FT ZN_FING 301 328 C2H2-TYPE (ATYPICAL).
 FT ZN_FING 334 358 C2H2-TYPE.
 FT ZN_FING 364 388 C2H2-TYPE.
 FT ZN_FING 394 416 C2H2-TYPE.
 FT DOMAIN 457 471 POLY-ALA.
 FT DOMAIN 491 509 POLY-GLY.
 FT VARIANT 471 471 A -> AAAAAAAAAA (IN HPE5).
 FT FTID-VAR 0088956 /FTID-VAR 0088956
 SQ SEQUENCE 533 AA; 55069 MM; CACFC90A31837C753 CRC64;
 Query Match 4.6%; Score 134.5; DB 1; Length 533;
 Best Local Similarity 35.5%; Pred. No. 0.21;
 Matches 38; Conservative 13; Mismatches 37; Indels 19; Gaps 3;
 QY 18 SASRRNL--HEMDEAQLPPASVG-----GGGSSSSAAAAAAAV 59
 DB 407 SLTRKHKHYESSPOGSESPRASSGESSTPPGLVSPSAEPQSSNLSPAAAAAA 466
 QY 60 SSSAPEIVSKPEHNNNNLALYGTGGGGGSGGGGGSGHSSSG 106
 DB 467 AAAAAVAHVHGGGSGG-AGGGSGGGSGGGGAGAGGGGGSSG 512
 RESULT 14
 CYAS RAT
 ID CYAS RAT
 AC 004400; STANDARD; PRT; 1262 AA.

DT 01-OCT-1993 (Rel. 27, Created)
 DT 01-NOV-1997 (Rel. 35, last sequence update)
 DT 30-MAY-2000 (Rel. 39, last annotation update)
 DE ADENYLATE CYCLASE, TYPE V (EC 4.6.1.1) (ATP PYROPHOSPHATE-LYASE)
 GN ADENYLATE CYCLASE.
 OS Rattus norvegicus (Rat).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 CX NBL_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=93028552; PubMed=1409703;
 RA Premont R.T., Chen J., Ma H.-W., Ponnappalli M., Iyengar R.;
 RT "Two members of a widely expressed subfamily of hormone-stimulated
 RT adenylyl cyclases".
 RL Proc. Natl. Acad. Sci. U.S.A. 89:9809-9813(1992).
 CC -1- FUNCTION: THIS A MEMBRANE-BOUND, CALMODULIN-INSENSITIVE ADENYLATE
 CC CYCLASE.
 CC -1- CATALYTIC ACTIVITY: ATP = 3',5'-CYCLIC AMP + PYROPHOSPHATE.
 CC -1- ENZYME REGULATION: INSENSITIVE TO CA(2+)/CALMODULIN. STIMULATED BY
 CC THE G PROTEIN BETA & GAMMA SUBUNIT COMPLEX.
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. CONTAINS TWO
 CC DOMAINS WITH 6 POTENTIAL TRANSMEMBRANE REGIONS EACH.
 CC -1- DOMAIN: COMPOSED OF TWO HOMOLOGOUS DOMAINS.
 CC -1- SIMILARITY: BELONGS TO ADENYLATE CYCLASE CLASS-4/GUANYLYL CYCLASE
 CC FAMILY.
 CC -----
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 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: M96159; AAB39764.1; -
 DR HSSP: P19754; IAWK.
 DR InterPro: IPR001054; -
 DR Pfam: PF00211; guanylate_cyc; 2.
 DR PROSITE: PS00452; GUANYLATE_CYCLASRS_1; 2.
 DR PROSITE: PS50125; GUANYLATE_CYCLASRS_2; 2.
 KW Lyase; cAMP synthesis; Transmembrane; Glycoprotein; Duplication.
 FT DOMAIN 1 242 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 243 263 POTENTIAL.
 FT TRANSMEM 269 289 POTENTIAL.
 FT TRANSMEM 300 320 POTENTIAL.
 FT TRANSMEM 326 346 POTENTIAL.
 FT TRANSMEM 351 371 POTENTIAL.
 FT TRANSMEM 375 395 POTENTIAL.
 FT TRANSMEM 396 763 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 764 784 POTENTIAL.
 FT TRANSMEM 790 810 POTENTIAL.
 FT TRANSMEM 837 857 POTENTIAL.
 FT DOMAIN 858 910 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 911 931 POTENTIAL.
 FT TRANSMEM 936 956 POTENTIAL.
 FT TRANSMEM 985 1005 POTENTIAL.
 FT DOMAIN 1006 1262 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 64 67 POLY-GLN.
 FT DOMAIN 141 147 POLY-ALA.
 FT CARBOHYD 871 871 N-LINKED (GLCNAC...) (POTENTIAL).
 FT CARBOHYD 888 888 N-LINKED (GLCNAC...) (POTENTIAL).
 FT CARBOHYD 973 973 N-LINKED (GLCNAC...) (POTENTIAL).
 SQ SEQUENCE 1262 AA; 139178 MM; 8B147E201C5D6601 CRC64;

Query Match 4.6%, Score 134.5, DB 1; Length 1262;
 Best Local Similarity 16.5%, Pred. No. 0.57;
 Matches 116; Conservative 61; Mismatches 206; Indels 243; Gaps 20;

3 SCRRNGVMPRLSNLSASRLNHEMSEAOPL----- 34
 53 STKRSGGAVTPQOORLASRRMGDDDEPLSGDDPLVGGFGFSRKSAMDERGDDG 112
 35 -----GASPSASAAAAAAVSSAPEIVYSKPEHNSNNLAL 81
 113 GNGSRQRGRAGAGGSTRAPAGSGSSAAAAAAGCTEVPREVEGLEERGGRAAE 172
 82 YETGGGGST--GGGGGGGGSGHSSGTSKSKKNNNIGYKGRRLFFKRRRLSDAL 139
 173 ELEPGTGVDDGGSGSSVYASGSGT----- 200
 140 IFMGEGIVVVIETELSMGAVDKASLYSLAKCLISLTIILGLIIVHAREIQLEFWD 199
 201 -----GTVLSTGA-----CCLAL-----LQIFRSK 220
 200 NGADDMRIAMTYERIF-----ICELIIVC-----AIHPIDGVYTTWTARLASYS 245
 221 KPPSD-KLERVQRYFFELROSSLTMLAVLVCLVLAFAAPPLQVYVLAVALA--- 276
 246 APTTADVDIILSLIP-----MFLRLYLIAVYL-----LHSLKPTDASSRSGA 290
 277 -----AAGVILIMAVLGNRAAFHODHMGACALIAVAVGVYVGLLPQRSASEGI 330
 291 LKINENTRPVMTLTICPGVLLVYSISIMIAAMVFRACERHQDQVTSNPLGAMW 350
 331 -----WVVFETITITLLP-----VR----- 347
 351 LISTFISIGYDMVPTNYCGKVCLLTGIMGAGTALVAVVAKLELTAKRHVNM 410
 348 -----MRAVLISGVL-----LSLHLAI-----SLHTVA 371
 411 MPTQLTRVKAANVLRBTWLLYNTKLYKKIDHAKVKKHOKRQLAIIHLSVMEGR 470
 372 QOQFLKQL--VSNV-----LIFSCINIVGCTHPRAVSRQAFQFOTRECIQARLSQ 423
 471 KLDQANTLVDLAKTONIMYDMISDLNERSD--FEKRIVTLETLETLGSIHALPGII 528
 424 RENQOGERLLSLVLRHVAMEKKADINAKQDMWFKIYIQKHNVSTLEFADIEGPTSLA 483
 529 SQTIRQOQROFIEQOMESYDKHVTYN 554
 484 SOCTAOELVMTLNELEPARFDKLAEN 509

RESULT 15
 CIRC_HUMAN STANDARD: PRT: 582 AA.
 ID CIRC_HUMAN
 AC 003721:
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 01-OCT-2000 (Rel. 40, Last annotation update)
 DE VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN KV3.4 (KSHIIC).
 GN KCNC4.
 OS Homo sapiens (Human).
 OC Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 CX NCBI_Taxid=9606;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=92396711; PubMed=1381835;
 RA Vega-Saenz de Miera E., Moreno H., Fruhling D., Kentros C., Rudy B.,
 "Cloning of Shit1 (Shaw-like) cDNAs encoding a novel high-voltage-
 RT activating, TEA-sensitive, type-A K+ channel.";
 RL Proc. R. Soc. Lond. B. Biol. Sci. 248:9-18(1992).
 CC -1- FUNCTION: THIS PROTEIN MEDIATES THE VOLTAGE-DEPENDENT POTASSIUM
 CC ION PERMEABILITY OF EXCITABLE MEMBRANES. ASSUMING OPENED OR CLOSED
 CC CONFORMATIONS IN RESPONSE TO THE VOLTAGE DIFFERENCE ACROSS THE

MEMBRANE, THE PROTEIN FORMS A POTASSIUM-SELECTIVE CHANNEL THROUGH
 CC WHICH K+ IONS MAY PASS IN ACCORDANCE WITH THEIR ELECTROCHEMICAL
 CC GRADIENT.
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
 CC -1- DOMAIN: THE SEGMENT 54 IS PROBABLY THE VOLTAGE-SENSOR AND IS
 CC CHARACTERIZED BY A SERIES OF POSITIVELY CHARGED AMINO ACIDS AT
 CC EVERY THIRD POSITION.
 CC -1- DOMAIN: THE TRAIL MAY BE IMPORTANT IN MODULATION OF CHANNEL
 CC ACTIVITY AND/OR TARGETING OF THE CHANNEL TO SPECIFIC SUBCELLULAR
 CC COMPARTMENTS.
 CC -1- SIMILARITY: THIS CHANNEL PROTEIN BELONGS TO THE DELAYED RECTIFIER
 CC CLASS. BELONGS TO SHAW POTASSIUM CHANNEL SUBFAMILY.
 CC -----
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 CC -----
 CC EMBL: M64676; AA57263.1; -;
 CC HSP: 063734; 127N.
 CC MIM: 176265; -;
 CC InterPro: IPR000636; -;
 CC InterPro: IPR003091; -;
 CC Pfam: PF00520; Ion_trans; 1.
 CC PRINTS: PR00169; KCHANNEL.
 CC Ionic channel; Transmembrane; Ion transport; Voltage-gated channel;
 CC Glycoprotein; Multigene family; Phosphorylation.
 CC DOMAIN 1 226
 CC TRANSMEM 227 247
 CC DOMAIN 248 277
 CC TRANSMEM 278 298
 CC DOMAIN 299 312
 CC TRANSMEM 313 333
 CC DOMAIN 334 380
 CC TRANSMEM 381 401
 CC DOMAIN 402 422
 CC TRANSMEM 423 443
 CC DOMAIN 444 451
 CC TRANSMEM 452 472
 CC DOMAIN 473 582
 CC CARBOHYD 256 265
 CC CARBOHYD 265 265
 CC SEQUENCE 582 AA; 64527 MW; 8E8E5AACA33A9F CRC64;

Query Match 4.5%, Score 134; DB 1; Length 582;
 Best Local Similarity 22.1%, Pred. No. 0.24; Indels 102; Gaps 20;
 Matches 89; Conservative 59; Mismatches 152;

39 SVGGGSGASPSASAAAAAAVSSAPEIVYSKPEHNSNNLALYGTGGGGGGGGG 98
 163 SPDGGSGAGSPDEAG-----DDERELALQRL-----GPHGG 195
 99 SGHSSGTSKSKKKNONIGYKGRRL--ALFE-----KRRRLDVA-LIFGMEGVVAV 150
 196 AGHAGSG-----GCGWOPRMKALFEDPSSAARVAFSLFELYSTTFC 244
 151 IETELSMGAVDKASLYSLAKCLISLTIILGLIIVHAREIQLEFWDNGADMRITAM 209
 245 LEHDAFN-IDR-----NVEILRVGNITSVHFREVEETPEI-----L 281
 210 TYER---IFFICELIVCAIHPICNTFT-----WTARLAFSAPSTTADVDIIL 258
 282 TYIEGVCVWMTTEFLV-RIVCCPTLDYFKNLIINDVALFLPELVGLSLSKAR 340
 259 SIMPELRLYLIAVYMLHSLKLETFDASSRSIGALNKINENTRPFVMTLTICPGVULVFS 318
 341 DYVLEGLRVRIVRILRFLRHFVGLRVLGHLTRASTV-EFL--DLIIFALAGVLFA 396
 319 ISWIIIAAMVFRACE-RYHDDQDVTSNPLGAMMULISITFLSIGDWMVPTVYCGK---GV 374

Typ May 15 08:41:27 2001

us-09-254-590-19.rsp

Page 13

Db 397 TMYYAERIGARPSDPRGNDHDPKNIPIGFWMAV-VTMTLGTGDMTPKTWSGMLVGA 455
QY 375 CLTGTGAGCTALV-----AVVARKLELTKAEKHV 406
Db 456 CALAGVLTITAMPVPVIVNNFGMYSLAMAKOLP-KKKKHV 496

Search completed: May 14, 2001, 20:41:58
Job time: 6803 sec

GenCore version 4.5
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OK protein - protein search, using sw model

Run on: May 14, 2001, 17:53:00 ; Search time 42.21 Seconds
(without alignments)
942.681 Million cell updates/sec

Title: US-09-254-590-19

Perfect score: 2954
Sequence: 1 MSSCRNGVMPRLSASRLHSEADNPQPPASVGGGGGASPSAAAAAAS 579
.....SSRRRRSSSTAPTSBSS

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 198801 seqs, 68722935 residues

Total number of hits satisfying chosen parameters: 198801

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2118.5	71.7	731	2	T09172
2	915	31.0	707	2	T24361
3	902	30.5	925	2	T18747
4	669	22.6	471	2	T15394
5	532.5	18.0	475	2	T20165
6	156.5	5.3	393	2	JC5275
7	133.5	5.2	924	2	B41359
8	151.5	5.1	744	2	T34116
9	150.5	5.1	924	2	S12746
10	147	5.0	489	2	JC4787
11	146.5	5.0	769	2	I56546
12	146	4.9	630	2	JU0271
13	144	4.9	484	2	T24238
14	142	4.8	679	2	A42073
15	141.5	4.8	1264	2	S41603
16	140.5	4.8	498	2	A41359
17	138.5	4.7	333	2	A39065
18	137.5	4.7	475	2	A43915
19	137	4.6	776	2	T20896
20	136.5	4.6	1718	2	T14603
21	136	4.6	455	2	A70461
22	135	4.6	490	2	A35312
23	135	4.6	645	2	T27186
24	134.5	4.6	497	2	JE0275
25	134	4.5	651	2	A39372
26	132.5	4.5	392	2	B48423
27	132	4.5	625	2	S13919
28	132	4.5	2248	1	D42088
29	131	4.4	1017	2	T31354

30	130	4.4	688	2	S55349	potassium channel
31	128.5	4.4	236	2	I57681	potassium channel
32	128.5	4.4	671	2	A35912	homoeotic protein e
33	128.5	4.4	1969	2	T08875	histidine kinase h
34	125.5	4.2	440	2	S71795	transcription fact
35	125.5	4.2	581	2	S17150	potassium channel
36	125.5	4.2	853	1	CHRTD1	potassium channel
37	125	4.2	427	2	A32372	female-specific doub
38	125	4.2	549	2	B32372	male-specific doub
39	123.5	4.2	857	2	I56529	potassium channel
40	123	4.2	592	2	B82759	endo-1,4-beta-gluc
41	122.5	4.1	1284	2	T13168	probable potassium
42	121.5	4.1	396	2	A45185	adenylylcyclase ty
43	121.5	4.1	613	2	A39402	potassium channel
44	121.5	4.1	624	2	S22703	voltage-gated pota
45	121.5	4.1	1184	2	A42904	adenylylcyclase ty

ALIGNMENTS

RESULT 1
T09172
probable calcium-activated potassium channel KCNN3 - human
C:Species: Homo sapiens (man)
C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 11-May-2000
C:Accession: T09172
R:Chandy, K.G.; Fanti, E.; Wittekindt, O.; Kalman, K.; Tong, L.L.; Ho, T.H.; Gutman
Mol. Psychiatry 3, 32-37, 1998
A:Title: Isolation of a novel potassium channel gene hSKCa3 containing a polymorphic
A:Reference number: 216601; PMID:98150774
A:Accession: T09172
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-731 <CH>
A:Cross-references: EMBL:AF031815; NID:g3309530; PID:g3309531
C:Gene: KCNN3
C:Genetics:
A:Keywords: potassium channel; schizophrenia

Query Match	71.7%;	Score 2118.5;	DB 2;	Length 731;
Best Local Similarity	73.7%;	Pred. No. 3e-137;		
Matches 427;	Conservative 48;	Mismatches 79;	Indels 25;	Gaps 3;
QY	1	MSSCRNGVMPRLSASRLHSEADNPQPPASVGGGGGASPSAAAAAAS	60	
DB	175	MSSCRNGVMPRLSASRLHSEADNPQPPASVGGGGGASPSAAAAAAS	213	
QY	61	SSAPEIVVSKPNNHNNALYGTGGGGGSGGSGGSSGSKSKKKKNGIKY	120	
DB	214	SNPEIVVSKPNNHNNALYGTGGGGGSGGSGGSGSKSKKKKNGIKY	269	
QY	121	LGHRALFEKKRRLSDYALIFMGVIVVITELSMCAVDKSLSLAKLISLSTII	180	
DB	270	LGHRALFEKKRRLSDYALIFMGVIVVITELSMCAVDKSLSLAKLISLSTII	329	
QY	181	LLGLIIVHAREIOLFVANGADPWRLAMTYERIFLLELVCALHPIPGVYTFWTAR	240	
DB	330	LLGLIIVHAREIOLFVANGADPWRLAMTYERIFLLELVCALHPIPGVYTFWTAR	389	
QY	241	LAFTYASTVVDYDITISIPMLRLYLARVMLHSLFTDSSSISGALKKINFTNR	300	
DB	390	LAFTYASTVVDYDITISIPMLRLYLARVMLHSLFTDSSSISGALKKINFTNR	449	
QY	301	VKTLMTICPGVLLVFSISLMTIAVYACERYHDOQVTSNFGAMWLISITFSLIG	360	
DB	450	VKTLMTICPGVLLVFSISLMTIAVYACERYHDOQVTSNFGAMWLISITFSLIG	509	
QY	361	YGDVWPVYTGKGVCLTIGMGACCTALVAVAVAKRLTFAEKVHNFMMDTQLTRVK	420	
DB	510	YGDVWPVYTGKGVCLTIGMGACCTALVAVAVAKRLTFAEKVHNFMMDTQLTRVK	569	

```

RESULT      2
T24361
hypothetical protein T02E1.8 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C:Accession: T24361
R:Lennarz, N.
submitted to the EMBL Data Library, November 1996
A:Reference number: Z19801
A:Accession: T24361
A:Status: preliminary; translated from GB/EMBL/DBD
A:Molecule type: DNA
A:Residues: 1-707 <Wtl>
A:Cross-references: EMBL:815181; PDB:1CB04662.1; GSPDB:GN00019; CESP:T02E1.8
A:Experimental source: Clone T02E1
A:Genetic:
A:Gene: CESP:T02E1.8
A:Map position: 1
A:Intons: 65/3; 295/1; 337/2; 364/3; 444/2; 586/3; 622/2; 645/3; 697/3

```

[illegible]

RESULT 3
 T18747
 Probable potassium channel protein - *Caenorhabditis elegans*
 C:Species: *Caenorhabditis elegans*
 C:Date: 15-Oct-1999 #sequence
 C:Accession: T18747; T26884
 R:Ainscough, R.
 submitted to the EMBL Data Library, November 1996
 A:Reference number: 219015
 A:Accession: T18747
 A:Status: preliminary; translated from GB/EMBL/DBD
 A:Molecule type: DNA
 A:Residues: 1-925 <M12>
 A:Cross-references: EMBL:281455; PIDN:GAB03807.1; GSPDB:GN00023; CESP:B0399.1
 A:Experimental source: clone B0399
 R:Ainscough, R.
 submitted to the EMBL Data Library, October 1998
 A:Reference number: 220279
 A:Accession: T26884
 A:Status: preliminary; translated from GB/EMBL/DBD
 A:Molecule type: DNA
 A:Residues: 1-925 <M12>
 A:Cross-references: EMBL:AL032637; PIDN:CAA21625.1; CESP:B0399.1
 A:Experimental source: clone Y43F8C
 C:Genetics:
 A:Gene: CESP:B0399.1
 A:Map position: 5
 A:Insertions: 39/1; 78/2; 113/3; 160/3; 205/1; 338/1; 388/2; 408/3; 441/3; 510/1; 563/3;

Query Match	Local Similarity	30.5%;	Score 902;	DB 2;	Length 925;
Best Local Similarity	35.3%;	Pred. No. 6,4e-54;			
Matches 195;	Conservative 116;	Mismatches 156;	Indels 86;	Gaps 107;	
Qy	61	SSAPPIYVSPKPE---	HNSNNMLALYTGCG-----	GGSTGGGGGGGG-----	98
Db	317	SKRRVAKISDPKQIIHIF	NYDRIVNGGVGREDNDVIE	STSGAASGGVGTPEKKIAGFR	376
Qy	99	---SCHGSSSGKSSKKRKN	ONIGKLGHRRALEFKRRRLSDV	ALLFGFGIVVMYIETEL	155
Db	377	RQSGSYGIAISSDSSTAK	KRCRL-----RKOLFRRKACD	ISFLAVLLIIVIIIDSEL	430
Qy	156	----SWGAVDKASVLSL	KCLKLSLSTIIILGLIIVYHARE	IQELPMYDNGADDMWRIMATY	211
Db	431	TALLSSGTGIRKDSPI	ITILRSACAVSTFPLICDILN	HAIEYKIALIDSADDMWRVAST	490
Qy	212	ERIFPICTELIVCAIHP	IPGQVYEFMTATNFAVSPT	-----TADVIIISIPMLR	265
Db	491	DFEIKMLIEVCOMCI	PPPELF--DGLMKPIYINAD	TRQYKKAHDVPIDVLSAPMFLR	547
Qy	266	LTILARWMLLHSLKLT	DDSSRISGALINKINFRFVAKT	LMTICPGVLLVFSISLMTIA	325
Db	548	STVLCRWVYHLSKOP	ADAAFRSITAIANLRISD	EFYIKTMADHDELIVLITFEL	5YNNACM 607
Qy	325	AMTVACERYHQDQVST	NFLGAMMLISITFLSIS	IGDVAWPVTCGKGVCLLTG	IMSGGC 385
Db	608	SMFETQOCERYPDQ	LEVEHYHLLNSMFIW	FMISIGRIDVPRITCGRCL	SITTTGIVAGV 667
Qy	386	TALVAVAVARKEIT	FKAEKRIHNMFMMDOL	KRYKRAAANULRETNLI	LYKNRKLAKYKTDH 445
Db	668	SSALLAIISKIELS	RAEKRYVNHFNMAKDS	KLNRCKRAAASVYDLE	THIRYKKAALHKGDD 727
Qy	446	AKYKHQRFLOALIH	QLSVYKMEQRKLNDQANT	VLDAKYONIWYDMSID	LNENSEDEFEK 505


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Db      728 LRHRHGRFLASINERFKIKWDQKLOEKNSILVYGLHSDMHELTLMEMHRTQDHFIS 787
      506 RIVTLETKLEFLIGSIALHGLISITINQOORDFEIAQWESYDKHVTYNAERSRSSRRR 565
      788 QIDVLTOKI-----MELQK-----TLNT----- 805

QY      566 RSSSTAPPTSSSES 578
      806 RPPCCAPPTSSSN 818

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RESULT 4
T15394
Hypothetical protein C03F11.1 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
C:Accession: T15394
R:Bentley, D.
submitted to the EMBL Data Library, October 1995
A:Description: The sequence of C. elegans cosmid C03F11.
A:Reference number: Z18342
A:Accession: T15394
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-471 <BEN>
A:Cross-references: EMBL:U39744; NID:g1049465; PID:g1049466; PIDN:AA80439.1; CESP:C03F11
A:Genetics:
A:Gene: CESP:C03F11.1
A:Introns: 21/1; 47/2; 71/2; 137/3; 174/1; 234/3; 336/3; 415/2

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Query Match      22.68; Score 669; DB 2; Length 471;
Best Local Similarity 34.3%; Pred. No. 2,4e-38;
Matches 156; Conservative 92; Mismatches 136; Indels 74; Gaps 13;

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QY      96 GGGSGHSSSGTKSSKKKKNQIG-----YKLGHRRLAFKRRKLSDYALIFGMP 144
      30 GSYVSHMTSS---AFGRNNSRYGVPIDSTAVKQYRVKSER--LTNRVRITDRSLYALF 84

QY      145 GIIVVMTIEELS---WGAIVDKASLYSLAKCLISITILLGLIIVYHAREIQLPMVDNG 201
      85 GVIIMLVESEITAEKFGVSKTWHISQSLVGVGTSTIALIYHILLHLNDLYELVDGCG 144

QY      202 ADDRIAMTERIFPCLIEIIVCAIHPIQNTYFTWTRALAFSVAAS----- 248
      145 ADMRWVVTTERVIOFCIEIPICGICPLPGSGEMKWT-----FIEPSLHNDGPSEKTVQ 199

QY      249 TTTAD--VDIISIPWFLRLYLIRVWLHLSKLPDASRSISGLKINFTFYKTIAM 306
      200 TRNDVDPVDVILSCFMLCSTLFAKFWLHSHKQFODASTRIALALNLIQVNTSFYKISL 259

QY      307 TICPGTVLVFSISLMIITAAVTACERY-----HDQDVTNFGAMWLISITELSGY 361
      260 DQGPVLELTFTFETFIWIIWSMFWOCERYGSGKNFOSILXN---SLMFIALTTEPLNGY 316

QY      362 GMPVNTYCGKGCGLTGLMGAGCALVAVARKELETKAEKHVHFMADTOLTRRYKN 421
      317 GDIVKQINAGRTAIFGVYGVAVISITILAVIRNLLISQGRVNNFVDSKLAREHE 376

QY      422 AAANLRETWLIYKNTKLVKID--HAKVRHQRKLOAIHQLSVYMEQRKINDQANTL 479
      377 AAARVLOHTWHIHI---KCLQSGDGGNRLRFLRYRKLKIHFRKSVKSEKME----- 425

QY      480 VDLAKTONIMYDMSIDLNESEDPEKRIYV--LETKLETLI 518
      426 -----FSENNQNNPQWTRLYTDMHTSMQRL 452

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RESULT 5
T20165
Hypothetical protein C53A5.5 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans

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C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C:Accession: T20165
R:Mortimore, B.
submitted to the EMBL Data Library, November 1996
A:Reference number: Z19232
A:Accession: T20165
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-475 <WIL>
A:Cross-references: EMBL:Z81486; PIDN:CA803986.1; CSDPB:GN00023; CESP:C53A5.5
A:Experimental source: clone C53A5
A:Genetics:
A:Gene: CESP:C53A5.5
A:Map position: 5
A:Introns: 23/1; 140/3; 177/1; 281/2; 295/3; 322/3; 359/2; 406/2

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Query Match      18.0%; Score 532.5; DB 2; Length 475;
Best Local Similarity 29.3%; Pred. No. 5.2e-29;
Matches 127; Conservative 96; Mismatches 190; Indels 21; Gaps 7;

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QY      99 SCHGSSSGTKSSKKKKNQIGYKLGHRRLAFKRRKLSDYALIFGKGVVMTIEELS-- 156
      43 SVYGRKYGVAMSNAEYRKRMKI--RRRLSDKVKLCDAITLLAVGILLMLDVEFTAF 100

QY      157 --WGAIVDKASLYSLAKCLISITILLGLIIVYHAREIQLPMVDNGADRIAMTYERI 214
      101 RILESIVNTSLSITLTAIITITALLPFLFHFIDIKQLVETGFSNRRVGTISERV 160

QY      215 FTICLEIIVCAIHPIQNTYFTWTRALAFSVAAPST--TTADVDIISIPWFLRYLIR 271
      161 LNTLEVALCALCPETGVAVAMP--TISNIAETRRRVNIPISVLILPFLFETVCR 218

QY      272 VMLHSLKLPDASRSISGLAKINFTFRVYKTIAMTICPGTVLVFSISLMIITAAVTARA 331
      219 YMLHSSQHDIAFRTIASLNHIAVDFRYLSEKRYRPLFYSLASLFWCSNMLAQ 278

QY      332 CERHQOQVYTNFPGAMWLISITELSGYGVMPNTYCGKGCGLTGLMGAGCALVA 391
      279 CER-----QILSHKKKQVLS--TFESIGYGVQVNTYCGRGLAMLTAVGLTFSSTLIA 332

QY      392 VVARKLELTRAEKHVHFMADTOLTRRYKNAAANYLRETWLIYKNTKLVKTI-----DHAK 447
      333 LISRKILITTCERKRVNHIITENNTEHNAACVLOMTRTVRLARDOQSSRRRQOR 392

QY      448 VRKHQRFLQAIHQLSYKMKORLNDQANTLVDLAKTONIMYDMSIDLNESEDPEKRI 507
      393 LAKMQRMLCSYITTRKTRKRLKMQMEDDEFTARRAFNFTEDRLQXVROQSOLDGKI 452

QY      508 VTLETKLETLIGSI 521
      453 SMLFENVEALTOAV 466

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RESULT 6
JC5275
Voltage-gated potassium channel protein - human
C:Species: Homo sapiens (man)
C:Date: 16-Apr-1997 #sequence_revision 09-May-1997 #text_change 05-Nov-1999
C:Accession: JC5275
R:Yokoyama, M.; Nishii, Y.; Yoshii, J.; Okubo, K.; Matsubara, K.
DNA Res. 3, 311-320, 1996
A:Title: Identification and cloning of neuroblastoma-specific and nerve tissue-specific
A:Reference number: JC5275; MUID:97191543
A:Contents: neuroblastoma cell
A:Accession: JC5275
A:Molecule type: mRNA
A:Residues: 1-393 <YOK>
A:Cross-references: DDBJ:D82346; NID:g1841341; PIDN:BA1157.1; PID:d1012224; PID:g18

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```

Query Match      5.3%; Score 156.5; DB 2; Length 393;
Best Local Similarity 20.6%; Pred. No. 0.0021;

```

Matches 93; Conservative 62; Mismatches 169; Indels 127; Gaps 20;

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OY 40 VGGGGGSSPSAAAAAIVSSAP--IVSKPEHNNSNNLALYGTGGGGGCGG 97
    ||| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 25 VGIDRQAPD-STRGALLLAGSEAPKRSILSKR-----AG 60
OY 98 GSGHSSSGTSKSKKNNQIGYKLGHRALPEKRLSDVALIFGMFIVVTELESM 157
    ||| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 61 GAGAGKPPKRNAPFRKLONFLYN-----VLERPKM 91
OY 158 GAYDKASLSLALCKLSLSTIIL-----GLIIVHAREIOLEFVNDGADNRIM 209
    ||| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 92 AFTHAYVFLVEFCLV-LSVSTKEKESSEBALYLEIIVIVEFV----- 140
OY 210 TYERFFICLEILVCAIHPIGNYTFWTARLASVAPSTTADVDIILSIPELRLYL 269
    ||| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 141 -----YFVRIMAGGCC-----RYR-GWRGRKFKARKPCV---IDIMV-----LI 177
OY 270 ARVMLL-----HSKLTDDASSRS-----IGALKKINFRFVAKTMTICPGVLLVS--I 319
    ||| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 178 ASIAVLAAGSGNVFATSLRSLRFLQILMMDRGGTWKLL---GSAVVAHSEKLY 233
OY 320 SLW-----ITAMTVRACERYHDODVTSNFGAMMLISITELSTIGDMVPNTYCGK 372
    ||| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 234 TAWIIGFLCLILASFLVLYAEK--GENDHEDTYADALMGLITLTIGCDKYPQTMGR 291
OY 373 GVCLLTIMGAGCTALVAVVARKLELTKAEKHVHFMMDQLTKRKNAANVIRETWL 432
    ||| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 292 LLAATFLLGVSEFALPAGISIGSFALKVQEDH-----ROKHFKR-RNPAGLIGSAMR 345
OY 433 IYKNTKLVKKIDHAKYRKORRFLQAIHOLR 463
    ||| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 346 FYA-TNLSRTDLHSTWYERTVTPMYR 375
    ||| | | | | | | | | | | | | | | | | | | | | | | | | | | |

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RESULT 7

B41359
potassium channel protein shab1 - fruit fly (*Drosophila melanogaster*)
C:Species: *Drosophila melanogaster*
C:Date: 03-Apr-1992 #sequence_revision 03-Apr-1992 #text_change 16-Feb-1997
C:Accession: B41359
R:Butler, A.; Wel, A.; Baker, K.; Salikoff, L.
Science 243, 943-947, 1989
A>Title: A family of putative potassium channel genes in *Drosophila*.
A:Reference number: A41359; WUID:89146139
A:Accession: B41359
A>Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tra
A:Molecule type: mRNA
A:Residues: 1-924 <RUT>
A:Cross-references: GB:M32659
C:Genetics:
A:Gene: flyBase:Shab
A:Cross-references: flyBase:FBgn0003183
C:Superfamily: potassium channel protein drk1

Query Match 5.2%; Score 153.5; DB 2; Length 924;
Best local similarity 19.3%; Pred. No. 0.01;
Matches 141; Conservative 85; Mismatches 222; Indels 281; Gaps 34;

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OY 38 ASVGGGGGSSPSAAAAAIVSSAPETIVSKPEHN--NSNNLALYGTG---GGSTG 92
    ||| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 175 ACTGTGTGAGSGSGSAGAGKEY-PYAP-FPYASPTHSITPTSOQIVGGVGVGASQ 232
    ||| | | | | | | | | | | | | | | | | | | | | | | | | | | |
OY 93 GGGGGSGHSSSGT-----KSKKKNQIGYKLG--HRRALF 128
    ||| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 233 STSGGVPTHSQSWTTCALDRHSRMSISPPPEFMIAQSAVSRVSNVGGVRHEVLM 292
    ||| | | | | | | | | | | | | | | | | | | | | | | | | | | |
OY 129 EKRRRL-----SDYA----- 138
    ||| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 293 RTLERLPTRLGRLECTTHEAIVELCDYSLADNEYFDNRHPSFSIINFRTGKLIH 352
    ||| | | | | | | | | | | | | | | | | | | | | | | | | | | |
OY 139 -----LIFG-----MFGIVVVIET-----ELSWG 158
    ||| | | | | | | | | | | | | | | | | | | | | | | | | | | |

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Db 353 VDEMCLAFGGDLEIYMWVDELTIESCCOHKHOKEKNEHREKRAESLRQDEEFEGG 412

OY 159 AYDKASLY-----SLAKCLISLSTI-ILLGLIIVHAREIOLEFVNDG--DDM 205

Db 413 KRSEYQKLMLELEKPNSTFAARVAVISILFIVLSTIALTLNPLQIHDNGTPODNP 472

OY 206 RIAMTYERIFICLEILVCAIHPIGNYTFWTARLASVAPSTTADVDIILSIPELRLYL 259

Db 473 OLAM-----VEAYCIT-----WTLLEYILRSSSPDKWFKKGLNIDILAI 515

OY 260 IMPELRLYL-----IARVMLLSKLTDDASSRSIGALKKI 294

Db 516 LFYEVSLELETKKNAADGQFQDVRVQVVERINRLIRLKL-----ARHSTGLSL 566

OY 295 NENTRFVAKTMTICPGVLLVFSISLIMITAMTVRACERYHDODVTSNFG---AMWL 351

Db 567 GFTLNSYKEL-----GLMLFLAMGVLISSIAV-----FAEKEDKTFVSIPEAFMW 616

OY 352 ISITELSIGDMVPNTYCGKGVCLLTIGAGCTALVAVVARKLELTKAEKHVHFM 411

Db 617 AGITMTTVGIRDICPTALGK-----YIGVCCICGVLLVLPILII-----VNNFAE 664

OY 412 DTOLTKRVKNAANVIRETWLYKN-----TKLVKKIDHAKV--RKHQREFLOAIHOLRSV 465

Db 665 -----FYKNQWREKALKRREHSIVPSGRQCHLLPSTYOSERSF 703

OY 466 KMEQRKLNQDANTLVDLAKTQNIIMYKIDSLNERSDEFEKRIYVLTLETIGSIHALP 525

Db 704 -----AKSMIDLIVDTGKQTNVHKK-----GRQSTPIGKQTL--DVQAP 746

OY 526 GLISQIRQOQDETEAOMES-----YDKHVTVAERSSRRSS--S 569

Db 747 G---HNLSDTQDNSTEGESTSGRNPAITGTGCKYKND--HVA-NLRNSNLNHRSSSEOD 801

OY 570 TAPPTSES 578

Db 802 AVPPYSFDN 810

RESULT 8

T34116
voltage-gated potassium channel klq-1 - *Caenorhabditis elegans*
C:Species: *Caenorhabditis elegans*
C:Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 18-Feb-2000
C:Accession: T34116
R:Milcox, L.
submitted to the EMBL Data Library, December 1995
A:Description: The sequence of C. elegans cosmid C25B8.
A:Reference number: Z21479
A:Accession: T34116
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-744 <WIL>
A:Cross-references: EMBL:U41556; PTDN:AAC70874.1; GSPDB:GN00028; CESP:C25B8.1
A:Experimental source: strain Bristol N2; clone C25B8
C:Genetics:
A:Gene: klq-1; CESP:C25B8.1
A:Map position: X
A:Introns: 31/3; 64/1; 81/3; 131/2; 161/3; 204/1; 262/3; 304/3; 341/3; 402/2; 426/1;

Query Match 5.1%; Score 151.5; DB 2; Length 744;
Best local similarity 19.7%; Pred. No. 0.01;
Matches 108; Conservative 90; Mismatches 192; Indels 159; Gaps 24;

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OY 11 MRPLSNLSASRNLHEMDESAQPLQPPASVGGGGGSSPSAAAAAIVSSAPETIVSK 70
    ||| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 15 MKRLSPVAVNYSRQKKTIDQAP-----SDRQAGASSSAIQEERKTVVPOE 62
    ||| | | | | | | | | | | | | | | | | | | | | | | | | | | |
OY 71 P-----EHNNSNNLALYGTGGGGGSGTGGGGGSGHSSSGTSKSKKKNQIGYKLGHR 124
    ||| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 63 PDIGFPEHDLQTLT-----HDSBEG-----NRKMSLVGKPLTYK 97
    ||| | | | | | | | | | | | | | | | | | | | | | | | | | | |

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Db 233 S1SGGVPHTS0NTGAL0RTHSRMSMS1PPPEPFMA0SKAVNSV1ANNGVHREVLN 292
QY 129 EKKERL-----SDYA-----138
Db 293 RTIERLPHRLRGLEGECTHEALIVELECDDBYSLADNEFFEDRHRKSPS1LNFYRGLKHI 352
QY 139 -----LIFG-----MGIYVAVIET-----ELSWG 158
Db 353 VDEKCVLAVGDDLEWGVDELYLESCCQKHQKRENVHEEMREKREASLRORDEEFGG 412
QY 159 AYDKASLY-----SLAKCLISLSTI--ILGLIYVHAREIOLFEPVNGA--DDW 205
Db 413 KSEYQKYLMELEKPNTSFAARIVAVISLFTVLSTLALNLFPLQLOHIDNGTPODNP 472
QY 206 RIATYERIFICELEILVCAIHPRGNYTFPTARLASVAPST-----TADVILIS 259
Db 473 QLAN-----VEAVOIT-----WPTLEYILRFSSSDKWKFFKGLNIIDLAI 515
QY 260 IPMELRLXL-----IARVWLHSLKFLTDASSRSGIALNKI 294
Db 516 LPFYVSJLLETKKNAITDPODVRVVOVPRIMIRILREVLKT-----ARHSTGLQSL 566
QY 295 NENTREYAKLTMTICGYVLVLFSSILMI1AAWTVBACERYHDOODVYSNFG--AMWL 351
Db 567 GTLLNSYKEL-----GLMLFLANGVILFISLAV-----FAEKDEKPTKVS1PEAFW 616
QY 352 ISIITFLSIGDWMVPNTYCGKVCGLLIGIMAGCITALVYAVARLELTREKREKVVHNFMM 411
Db 617 AGITVTYTGIDICPTTALGK-----VITVCCICGVLYVALPPII-----VNNF-- 662
QY 412 DPOLKRRVKNAAVULRETLIYKTKLVKIKIDHAVKRHQRKELOAIHOLSRKMQRK 471
Db 663 -----AEFKN--QMRRE--KALKRREALDRAK-----REGSIVSFFHI--NLKDAFAK 705
QY 472 LNDQANTVLDLAKQONIMYDMISDLNERSGEDEKRIYTLFETKLETLIGSIHALPGLISOT 531
Db 706 SMLDLIDVYDGKOTNVHPR-----GKNOSFPNIGROT--DVOSAP--HN 749
QY 532 IROQOQDFLEAOMES-----YKHVHYNAKSSRRSSRRRRSS--STAPPTS 575
Db 750 LSGDGNSTEGESTSGRNPATITGCKYKNID--HVA--NLNRSNLNHRGSSSDODAVPYS 807
QY 576 SES 576
Db 808 FDN 810

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RESULT 10

JC4787
shaw protein - California spiny lobster

C:Species: Penulirus interruptus (California spiny lobster)

C:Date: 10-May-1996 #sequence_revision 16-Aug-1996 #text_change 08-Dec-2000

C:Accession: JCA4787

R:Baro, D.J.; Cole, C.L.; Harris-Warrick, R.M.

Gene 170, 267-270, 1996

A:Title: The lobster shaw gene: Cloning, sequence analysis and comparison to fly shaw

A:Reference number: JCA4787; MUID:96235147

A:Accession: JCA4787

A:Molecule type: mRNA

A:Residues: 1489 <BAR>

A:Cross-references: GB:148691; NID:q1100226; PID:q1100227

A:Comment: This protein is a voltage-dependent potassium (K+) channel protein.

C:Genetics:

A:Gene: shaw

C:Superfamily: potassium channel protein drkl

C:Keywords: membrane protein; phosphoprotein; transmembrane protein

F:171-190/Domain: transmembrane #status predicted <TM1>

F:226-248/Domain: transmembrane #status predicted <TM2>

F:260-280/Domain: transmembrane #status predicted <TM3>

F:291-311/Domain: transmembrane #status predicted <TM4>

F:324-342/Domain: transmembrane #status predicted <TM5>

F:387-410/Domain: transmembrane #status predicted <TM6>

F:10_190/Binding site: phosphate (Thr) (covalent) (by calmodulin-dependent kinase II)

E:19,41,48,86,140,163,228/Binding site: phosphate (Tyr) (covalent) #status predicted
 E:22,66,316,475/Binding site: phosphate (Thr) (covalent) (by protein kinase C) #status
 E:126,157,281,320/Binding site: phosphate (Ser) (covalent) (by casein kinase II) #status
 E:320,483/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status predicted

Query Match
 Best Local Similarity 5.0%; Score 147; DB 2; Length 489;
 Matches 86; Conservative 38; Mismatches 131; Indels 110; Gaps 16;

QY 144 FGIIVVVIETELSGAVNDASISLSL-----ALCLISLSTILLGLIIVHARE--- 192
 DB 134 FGEEDYSSNLSMOKTPEKLSLEDEPYSSQAARVIVISVFICVSLSCCKTHHD 193
 QY 193 -----IOLEWYDNGAD-----DMRIAMTERIERFF-CL-----ELVCAIHPICGNY 233
 DB 194 MRVPIQNTVOTAEVNTTAMTLDKKATNAHEAFYIECVNMTFFELIRLT-ASPKRF 252
 QY 234 TF-----TWTFARLAF-----STASTTADVDIILSIPEFLRLYLARVMLHSK 278
 DB 253 MELKASVNMIDFATLSFYVDILQKFAHLENADILEFFSIIRIMRLELTR---HSS 308
 QY 279 LFTDASSRIGALKINKINENTREFVKTLCPCFVLVFSISLMI-IAAMTVRACERY-- 335
 DB 309 -----GKILITOTFRASAKELTLVFLVLCIYFASLVYAEIRIQ 350
 QY 336 HDQDVTNFIAGMMLISITFLSIGDWPNTYCGKVCCLTGINGACCAALVAVAVAR 395
 DB 351 NPHNDNSIFPLGLMVAL-VMTITVCGDAPRTYVGMFVALCALAGVLTALPVI-- 407
 QY 396 KLELTAKKHVHNFMMDTOLTRKVVNAANVLRFTWLYKNFTLVKIKIDHAKVKRHKRF 455
 DB 408 -----VSNFRM-----YSHMQA-----RAKLKKRRRY 431
 QY 456 LQAIH 460
 DB 432 LVEYH 436

RESULT 11

I56546
 Shaw type potassium channel - mouse
 C:Species: Mus sp. (mouse)
 C:Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 05-Nov-1999
 C:Accession: I56546
 R:Goldman-Wohl, D.S.; Chan, E.; Baird, D.; Heinzel, N.
 J. Neurosci. 14, 511-522, 1994
 A:Title: Kv3.3b: a novel Shaw type potassium channel expressed in terminally differentiated
 A:Reference number: I56546; MUID:94132879
 A:Accession: I56546
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-769 <RES>
 A:Cross-references: GB:S69381; NID:9545228; PIDN:AAC0607.1; PID:g545229
 A:Gene: Kv3.3b

Query Match
 Best Local Similarity 5.0%; Score 146.5; DB 2; Length 769;
 Matches 87; Conservative 47; Mismatches 134; Indels 123; Gaps 19;

QY 83 GTCGGG-----STGGGGGGGGSGHSSGSKSSKKKNQIGVKLGHR--- 125
 DB 229 GAGGGGDLGAGGELKRLCFQDAGGAGGLPGAGAGAGGT-----WHRKQP 274
 QY 126 ---ALFER--RKRLSDYALIFGEGIVVWVETELSGAVNDASISLSLSTII 180
 DB 275 RWMALFEDPYSSRAARYVAFASLPEI-----DISITTEFC 308
 QY 181 L---LGLIIVHAREIQLPMVNDGADWRAMTYERIEFTCLLEIVCAIHPICGNTFTW 237
 DB 309 LETHEGFHISNKTIVQASPIGAPENITNVEETEFLLYVAGCVVW-----FTTEF 363

QY 238 TARLAF-----SYASTTADVDIILSIPEFLRLYLARVMLHSKLEFTDASSRIGALN 292
 DB 364 LMRVTFPCDKWEFLKSSLNT-IDCVAILPEYLEVGL-----SGLSKRAADVIGFLR 414
 QY 293 KINF-----NTRFVKTLMTICPGVTLVFSISLMI-IAAMTVRACERY-H 336
 DB 415 VRFVRIILRLEKLRHFFVGLRVGLTLASNGEFLITLITLALGVLFAMTYAERIGA 474
 QY 337 DQDQVT-SNF-----LGAMLLSITFLSIGDWPNTYCGK---GVCILGIMGAGC 385
 DB 475 DDDIILSNHTYKPIEFKPMAN-VMTITVCGDWPRTYVGMFVALCALAGVLTALPVI 533
 QY 386 TALVY-----AVARKLELTAKKHV 406
 DB 534 PVPVIVNFGMYYSILAMAKRLP-KKKKKHI 563

RESULT 12

JU0271

voltage-sensitive potassium channel protein [validated] - rat
 N:Alternate names: rat shal1
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 01-Dec-2000
 C:Accession: JU0271; A39113
 R:Balwin, T.J.; Tsaur, M.L.; Lopez, G.A.; Jan, Y.N.; Jan, L.Y.
 A:Title: Characterization of a mammalian cDNA for an inactivating voltage-sensitive K
 A:Reference number: JU0271; MUID:92000693
 A:Accession: JU0271
 A:Molecule type: mRNA
 A:Residues: 1-630 <BAL>
 A:Cross-references: GB:S64320; NID:9236196; PIDN:AAB19939.1; PID:g236197
 A:Experimental source: hippocampus
 R:Roberts, S.L.; Tamkun, M.M.
 Proc. Natl. Acad. Sci. U.S.A. 88, 1798-1802, 1991
 A:Title: Cloning and tissue-specific expression of five voltage-gated potassium chan
 A:Reference number: A39113; MUID:9116694
 A:Accession: A39113
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-476, 'T', 'P', 603-604, 'ASL', 608, 'GENHE', 614 <ROB>
 A:Cross-references: GB:M59980; NID:g203467; PIDN:AAA40929.1; PID:g203468
 A:Description: this protein forms a 4-amino-pyridine-sensitive potassium channel [val
 F:38/Binding site: channel-forming protein; ion channel: phosphoprotein; potassium channel
 E:54,280,489,606/Binding site: phosphate (Thr) (covalent) (by CAMP- and GMP-dependent kinases) #
 E:70,447,531,537,548/Binding site: phosphate (Thr) (covalent) (by casein kinase II) #stat
 E:101,166,291,316/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #
 E:113,263,459,460,472,502,552/Binding site: phosphate (Ser) (covalent) (by casein kin
 E:592/Binding site: phosphate (Tyr) (covalent) #status predicted

Query Match
 Best Local Similarity 4.9%; Score 146; DB 2; Length 630;
 Matches 89; Conservative 61; Mismatches 134; Indels 120; Gaps 19;

QY 214 IFETCLEIVCAIHPICGNTFTWTFARLAFSAPS-----TTADVDIILSIPEFLRLY 267
 DB 227 VAFELDTACVMI-----FTVEYLRLA--AAPSRYRVSWSIIDVAIIPYIGLV 278
 QY 268 LI-----ARVMLHSKLEFTDASSRIGALKINKINENTREFVKTLCPCFVLVFSIS 320
 DB 279 MNDNEDWSGAFVTLRVERF-----RIFFSHSGGLRITGYTLKSCASELGFLESLT 332
 QY 321 LMIITAMTVRACERYHDQDVTNFI-----GAMLLSITFLSIGDWPNTYCGK---GV 374
 DB 333 MAIITFAVTFV---YAEKSSASKFSIRPATRYITVMTITVCGDWPRTYVGMFVALCALAGVLTALPVI 389
 QY 375 CLTIGINGACCAALVAVAVARKLELTAKKHVHNFMMDTOLTRKVVNAANVLRFTWLY 434
 DB 390 CSLSGVL---VIALFPVI-----VSNF----- 409

OY 435 KNTKLYKIDHAKYKHKRFLQAIHQKSKYKQKRLDQANTLVIAKTQNTIMYDMS 494
 Db 410 --SRIYHONORADKRRKOKK--ARARIRAK-----SGSAN-----AYWOSKRNGLIS 454
 OY 495 DINESEED---FEKRIVLETKLETLELIGSHALPGISQTRQOORFIEAQM--ESYD 548
 Db 455 NQLOQSEDEPAFVSKSSSPFQHHLL--LHCLF-----KTNHEFVDEQVFESECM 504
 OY 549 KHYTYNAERSRS-----SSRRRSSTAPPPSSSS 579
 Db 505 EYATYVRRSHSPSLSSQOQVYSTCCSRRAKKSFRIPNANVGS 548

RESULT 13

24238
 hypothetical protein R186.5 - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 08-Dec-2000
 C:Accession: T24238
 R:Barlow, K.
 submitted to the EMBL Data Library, August 1996
 A:Reference number: Z19861
 A:Accession: T24238
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-484 <WIL>
 A:Cross-references: EMBL:Z78016; PIDN:CA801442.1; GSPDB:GN00023; CESP:R186.5
 A:Experimental source: clone R186
 C:Genetics:
 A:Gene: CESP:R186.5
 A:Map position: 5
 A:Insertions: 30/2; 65/2; 85/3; 128/3; 235/3; 370/3; 409/3; 446/1
 C:Superfamily: potassium channel protein dir1

Query Match 4.9%; Score 144; DB 2; Length 484;
 Best Local Similarity 23.3%; Pred. No. 0.02;
 Matches 77; Conservative 40; Mismatches 104; Indels 110; Gaps 16;

OY 157 WGAYDKASLSIALKCLISITILLGLIY----- 188
 Db 156 WRLDEPN--SRSAQFIATISVFELTAIVFCLKTHPGRLPELAPGNRNHSTSS 214
 OY 189 --HAREIOLFVNDGADDMRIAMTERIFELIILVCAIHPNPTFTARLAESYA 246
 Db 215 RIHPAQINIDKANS-----RPHPTMYETIC-----NIMFTIELIARFSSC 256
 OY 247 PS-----TTADYDIIISIPMF-----LRTYLIRVWLLSKIFTDASS 285
 Db 257 PSREYELRAPVNIIDIVATLFYIDLSS--MGATADLEFFSILIRIM---RLF----- 305
 OY 286 RSIGALNKINFTREVKMTIMTCPGTVLVFSSISLMI--AMTVACERYHDOO--VY 342
 Db 306 ----KLTHNSGLKILMHTFRASAKELMLVFLVGVVAFSLVYAEVERESNEDQPF 361
 OY 343 SNLGLAMMLISTFELSIGDMPNRYCGK---GVCLLIGIMAGCTLVAAYVAKLEI 399
 Db 362 SIPIGLMAWI-VMTTIGYGDITPHYVIGRLIGISICALAGV--TIALPVL----- 411
 OY 400 TKAKEHVNFMW---DTOLTKRYKNAANVL 427
 Db 412 -----VSNFAMFYSHTOARSKMKPKRRGVL 436

RESULT 14

A42073
 potassium channel protein Kv3.3 - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 14-May-1993 #sequence_revision 14-May-1993 #text_change 05-Nov-1999
 C:Accession: A42073; S22046
 R:Ghanshani, S.; Pak, M.; McPherson, J.D.; Strong, M.; Dechlefs, B.; Wasmuth, J.J.; Salik
 Genomics 12, 190-196, 1992

A:Title: Genomic organization, nucleotide sequence, and cellular distribution of a Sh
 A:Reference number: A42073; MUID:92155707
 A:Accession: A42073
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-679 <GHA>
 A:Cross-references: GB:X60796; NID:g53759; PIDN:CAA43209.1; PID:g817994; GB:X60797

Query Match

4.8%; Score 142; DB 2; Length 679;
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 Matches 84; Conservative 52; Mismatches 139; Indels 108; Gaps 19;

OY 83 GTGGGGGTGGG-----GGGGSGH--GSSSGTKSSKKKQNTIGYKGRALFEK 130
 Db 152 GAGGGGIDGAGGELKRLCFQDAGAGDLPGARAAATWRRMQPRV-----ALPED 204
 OY 131 --RKLSDYALIFGMGYVWVITELSWGATYKASLSIALKCLISITIL--LGLI 185
 Db 205 PYSSRAARYVAFASLFFI-----LITTFECLETHEGFI 238
 OY 186 IYHAREIOLFVNDGADDMRIAMTERIFELIILVCAIHPNPTFTARLAES-- 243
 Db 239 HISNKTVAQSPIPGAPENITNVEVEEPLTYGCVVW----FTPEFLMRYTFCP 293
 OY 244 ----STABSTTADYDIIISIPMFELIILVCAIHPNPTFTARLAES-- 296
 Db 294 DKVEFLKSLINI-IDCVALLPYLEVGL-----SGLSKAADVLGLRVRVRVIL 344
 OY 297 ----NTRFVKMTIMTCPGTVLVFSSISLMI--IAATVACERY-HDOQDPT-S 343
 Db 345 RIFKLRHFGVLRVGLHTLRASTNEFLIILFALGVLFAMIVYERIGAPDDILGS 404
 OY 344 NF-----LGAAMLSTIFELSIGDMPNRYCGK---GVCLLIGIMAGCTALV-- 390
 Db 405 NHTYKNIPIGFMWAV-VMTTIGYGDMPKTVSGMLVGGICALAGVLTAMPVPIVNN 463
 OY 391 -----AVVAKLELTKAEKV 406
 Db 464 FGWYSLAMAKOKLP-KKKKKH 485

RESULT 15

S41603
 type V adenylyl cyclase - rabbit
 C:Species: Oryctolagus cuniculus (domestic rabbit)
 C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 16-Jul-1999
 C:Accession: S41603
 R:Malach, J.; Droste, M.; Kluxen, F.W.; Pfeuffer, T.; Frank, R.
 FEBS Lett. 338, 257-263, 1994
 A:Title: Molecular cloning and expression of a novel type V adenylyl cyclase from rab
 A:Reference number: S41603; MUID:94139935
 A:Accession: S41603
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-1264 <WAL>
 A:Cross-references: GB:Z29371; NID:g456756; PIDN:CA82562.1; PID:g456757
 C:Superfamily: human adenylyl cyclase; guanylate cyclase catalytic domain homology
 F:414-649/Domain: guanylate cyclase catalytic domain homology <GCC>
 F:1022-1261/Domain: guanylate cyclase catalytic domain homology <GCC>

Query Match 4.8%; Score 141.5; DB 2; Length 1264;
 Best Local Similarity 19.7%; Pred. No. 0.098;
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OY 20 SRRLHEHDSQQLDPPASVGGGGGASPSAAAAAASAAPELYSKPENNHNLU 79
 Db 118 SRORRGAAGGSTRAPAGCGGG---SAAAAAGTEVRRSYELGLEERGGGR 173
 OY 80 ALYGTGGGSGTG-GGGGGSGHSSGTSKSKKQNTIGYKGRALFEKRRRLSDYA 138
 Db 174 AVDELEAGAVYGGGAGDEGSSADSNSNP----- 202

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OY .139 LIFGMFGIVVNIETELSGVADKASLSLAKCLISLSTIILGLIIVYHAREIOLFMV 198
Db 203 -----GAV-----LSTGA-----CCAL-----LQIFRS 221
OY 199 DNGADDMRIAMTYERIFE-----ICLEIIVCAIHPIPGNTFTWTARLAFSYP 248
Db 222 KKEPSP-KIERLYQRYEFRLNQSLSLMAVPLVCLV-----MLAFHARP 267
OY 249 TTTADVOIILSIPELRLYLIAVMLHSLFTDASSRSIGALNKINFNTRFVYKTLMTI 308
Db 268 P-----LOLPLYLAVLAAGVILYMAVLCNRA-----FHODHMGCLA 304
OY 309 CPQTVLVEISISLMIAMTVRACERYHDQDVTSNFLGAMMLISTFSLISYGDWVPNT 368
Db 305 CYALLAVVLAQVVGILLPPRSASE-----GIMW--IVFFIITY-TLP-- 347
OY 369 YCGKGVCLTIGMGAGCTALVAVAVARKLELTKAEKHVHNMKMDTQLTRVKNAAANVLR 428
Db 348 -VEMRAAVLSGVL--LSTLHLAIALR--TNAQ--DRFL--KOLVSNV-- 386
OY 429 EFWLIYKNTKLVKKIDHAKVRKHORRFLQAIHOLRSVKMEORRUNDQANTLVDAKTONI 488
Db 387 ---LIFSCNIVGCTHYPAEVSQNAQFQETRECIOARLHSORENOOERLLSVLRHY 443
OY 489 MYDMISDLNERSD--FEKRIYVLETKLETIGSIALPGLISQITIROOORPTEAOMES 546
Db 444 AMEMKADINAKOEDMMFHKIYIQKHNVSLFADIEGFTSLASOCTAOELVMTLNLFLAR 503
OY 547 YDKHVTYN 554
Db 504 FDKLAEN 511
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Search completed: May 14, 2001, 18:49:30
Job time: 3390 sec

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 34 euGlnProProAlaSerValGlyGlyGlyGlyGlyAlaSerSerProSer 50
 558 TCGACCCCGCCGCTCTCTCGAGAGAGTGGCGGCGCTCTCCCGCT 607
 51 AlaAlaAlaAlaAlaAlaAlaAlaValSerSerSerAlaProGluLeu 67
 608 CGAGAGCTGCGCGCGCGCGCTCTCTCTCTCTCTCTCTCTCTCTCT 657
 67 ValSerSerProGluHisAsnSerSerSerSerSerSerSerSerSer 84
 658 GGTGCTTACGCGCGCGAGACACACACTCCAAACACCTGGCGCTTATG 707
 84 hGlyGlyGlyGlySerThrGlyGlyGlyGlyGlyGlyGlyGlyGly 100
 708 CCGCGCGCGGAGGAGACACTGAGAGAGCGCGCGCGCTGAGGAGCG 757
 101 HisGlySerSerSerGlyThrLysSerSerLysLysAsnGlnAsn 117
 758 CAGGCGACGAGAGTGGACCAAGTCCAGCAAAAGAAAACAGAACT 807
 117 eGlyThrLysLeuGlyHisArgArgAlaLeuPheGluLysArgLys 134
 808 CGGCTACAGCTGGGGCACCGCGCGCGCTCTCTCTCTCTCTCTCT 857
 134 euSerAspTyrAlaLeuLeuPheGlyMetPheGlyLeuValMetVal 150
 858 TCAGGCACTACCGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 907
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 908 ATGAGACCGAGAGCTGTCTGGGGCGCTCTCTCTCTCTCTCTCT 957
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 484 yThrGlnAsnIleMetTyrAspMetIleSerAspLeuAsnGluArg 500
 1908 AGACCAACATCATCATGATGATGATGATGATGATGATGATGAT 1957
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 1958 GAAGACTTCGAAAGAGATTTTATCCCTGGAACAAACTAGAGACT 2007
 517 uIleGlySerIleHisAlaLeuProGlyLeuIleSerGlnThrLeuArg 534
 2008 GATTTGATGATCTCAGCGCTCTCTCTCTCTCTCTCTCTCTCTCT 2057
 534 IingGlnArgAspPheIleGluAlaGlnMetGlySerTyrAspLysHis 550
 2058 AGCAGCAGAGATTTTATGAGCTCAGTGAAGTGAAGTGAAGTGA 2107
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seq_documentation_block: 1743 bp

LOCUS: RR069882

DEFINITION: Rattus norvegicus calcium-activated potassium channel rsk2 (SK)

ACCESSION: U69882

VERSION: U69882.1

KEYWORDS: GI:1575662

SOURCE Norway rat.
 ORGANISM Rattus norvegicus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
 Rattus.
 REFERENCE 1 (bases 1 to 1743)
 AUTHORS Kohler, M., Hirschberg, B., Bond, C. T., Kinzie, J. M., Marillon, N. V.,
 Maylie, J., and Adelman, J. P.
 TITLE Small-conductance, calcium-activated potassium channels from
 mammalian brain
 JOURNAL Science 273 (5282), 1709-1714 (1996)
 MEDLINE 96376602
 REFERENCE 2 (bases 1 to 1743)
 AUTHORS Bond, C. T., Maylie, J., and Adelman, J. P.
 TITLE Direct Submission
 JOURNAL Submitted (09-SEP-1996) Vollum Institute, Oregon Health Sciences
 University, 3181 SW Sam Jackson Park Road, Portland, OR 97201-3098,
 USA

FEATURES

Source

Location/Qualifiers
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 Ratio: 5.032 Gaps: 3
 Percent Similarity: 98.459 Percent Identity: 97.945

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Align seg 1/1 to: RRU69882 from: 1 to: 1743

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DEFINITION Gallus gallus small-conductance calcium-activated potassium channel
ACCESSION AF079372
VERSION AF079372.1 GI:6650273
KEYWORDS
SOURCE
ORGANISM
Chicken.
Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
1 (bases 1 to 2237)
REFERENCE
AUTHORS Zidanic M. and Fuchs P. A.
TITLE Small conductance calcium-activated potassium channel expressed in
JOURNAL chick cochlear hair cells
REFERENCE
AUTHORS 2 (bases 1 to 2237)
Zidanic M. and Fuchs P. A.

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TITLE Direct Submission
JOURNAL Submitted (20-JUL-1998) Otolaryngology - HNS, Johns Hopkins
University, 720 Rutland Avenue, Baltimore, MD 21205, USA
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Align seg 1/1 to: AF079372 from: 1 to: 2237

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ACCESSION AJ251016 GI:6453381
VERSION AJ251016.1
KEYWORDS calcium-activated potassium channel; K3 (KCNN3) gene; SK3 protein.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Primates; Catarrhini; Hominoidea; Homo.

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1 (bases 1 to 3095)
AUTHORS Verstappen,G.C., Pula,G., Chen,M.X. and Roncarati,R.
JOURNAL Unpublished
REFERENCE
2 (bases 1 to 3095)
AUTHORS Chen,M.X.
JOURNAL Direct Submission
Submitted (15-NOV-1999) Chen M.X., Molecular Pharmacology,
GlaxoWellcome Medicines Research Center, Gunnels Wood Road,
Stevenage, Herts, SG1 2NY, UNITED KINGDOM

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Alignment scores:
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DEFINITION Rattus norvegicus calcium-activated potassium channel rsk3 (SK)

ACCESSION U69884

VERSION U69884.1 GI:2564071

KEYWORDS

SOURCE

ORGANISM

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AUTHORS

TITLE

JOURNAL

MEDLINE

REFERENCE

AUTHORS

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JOURNAL

COMMENT

FEATURES

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CDS

BASE COUNT

ORIGIN

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US-09-254-590-19 x RU69884

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Page 11

KEYWORDS	VERSION
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ORGANISM	human.
REFERENCE	Homo sapiens
AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 2521) Chandy,K.G., Pantino,E., Wittekindt,O., Kalman,K., Tong,L.-L., Ho,T.-H., Gutman,G.A., Crocq,M.-A., Ganguli,R., Nimgaonkar,V., Morris-Rosendahl,D.J. and Gargus,J.J. Isolation of a novel potassium channel gene hSKCa3 containing a polymorphic CAG repeat: a candidate for schizophrenia and bipolar disorder? Mol. psych. 3, 32-37 (1998)
TITLE	2 (bases 1 to 2521)
JOURNAL	Chandy,K.G., Pantino,E., Wittekindt,O., Kalman,K., Tong,L.-L., Ho,T.-H., Gutman,G.A., Crocq,M.-A., Ganguli,R., Nimgaonkar,V., Morris-Rosendahl,D.J. and Gargus,J.J. Direct Submission Submitted (29-OCT-1997) Physiology and Biophysics, University of California at Irvine, Irvine, CA 92697, USA
REFERENCE	3 (bases 1 to 2521)
AUTHORS	Chandy,K.G., Pantino,E., Wittekindt,O., Kalman,K., Tong,L.-L., Ho,T.-H., Gutman,G.A., Crocq,M.-A., Ganguli,R., Nimgaonkar,V., Morris-Rosendahl,D.J. and Gargus,J.J. Direct Submission Submitted (13-JUL-1998) Physiology and Biophysics, University of California at Irvine, Irvine, CA 92697, USA
REMARK	Sequence update by submitter
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SOURCE     Mus musculus
ORGANISM   Mus musculus
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AUTHORS    Shmukler,B.E., Bond,C.T., Bruening-Wright,A., Maylie,J.,
            Adelman,J.P., and Alper,S.L.
TITLE      Molecular Cloning of Murine Potassium Channel MSK1
JOURNAL    2 (bases 1 to 2998)
AUTHORS    Shmukler,B.E., Bond,C.T., Bruening-Wright,A., Maylie,J.,
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TITLE      Direct Submission
JOURNAL    Submitted (23-DEC-1998) Molecular Medicine, Beth Israel Deaconess
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AUTHORS	Rattus.	
JOURNAL	Joiner M.J., Wang L.Y., Tang M.D. and Kaczmarek L.K.	
MEDLINE	HSK4, a member of a novel subfamily of calcium-activated potassium	
REVIEW	channels	
PROJ.	Proc. Natl. Acad. Sci. U.S.A. 94 (20), 11013-11018 (1997)	
CHANNELS	97454570	
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Joiner M.J., Wang L.Y., Tang M.D. and Kaczmarek L.K.		
Direct Submission		
Submitted (23-APR-1997) Pharmacology, Yale University, 333 Cedar		
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 mRNA, partial cds.
 ACCESSION U69885
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 SOURCE Norway rat.
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 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
 Rattus.
 1 (bases 1 to 1377)
 Kohler, M., Hirschberg, B., Bond, C.T., Kinzie, J.M., Marrion, N.V.,
 Maylie, J. and Adelman, J.P.
 Small-conductance, calcium-activated potassium channels from
 mammalian brain
 JOURNAL Science 273 (5282), 1709-1714 (1996)
 MEDLINE 96376602
 REFERENCE 2 (bases 1 to 1377)
 AUTHORS Bond, C.T., Maylie, J. and Adelman, J.P.
 TITLE Direct Submission
 JOURNAL Submitted (09-SEP-1996) Vollum Institute, Oregon Health Sciences
 University, 3181 SW Sam Jackson Park Road, Portland, OR 97201-3098,
 USA
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DEFINITION Rattus norvegicus intermediate conductance Ca2+-activated K+
channel (RIK1) mRNA, complete cds.
ACCESSION AF156554
VERSION AF156554.1 GI:5031525
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SOURCE Norway rat.
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
REFERENCE
1 (bases 1 to 1910)
AUTHORS Rajendran, V.M., Sangen, P., Joiner, W.J. and Binder, H.J.
TITLE CDNA cloning of an intermediate conductance Ca2+-activated K+
channel (RIK1) and its regulation by dietary K-depletion in rat

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JOURNAL distal colon
REFERENCE unpublished
AUTHORS 2 (bases 1 to 1910)
TITLES Rajendran, V.M., Sangen, P., Joiner, W.J. and Binder, H.J.
JOURNAL Direct Submission
Submitted (03-JUN-1999) Internal Medicine, Yale University, 333
Cedar Street, New Haven, CT 06520-8019, USA
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AUTHORS	1 (bases 1 to 1899)	
TITLE	Neylon,C.B., Lang,R.J., Fu,Y., Bobik,A. and Reinhart,P.H.	
JOURNAL	Molecular cloning and characterization of the intermediate-conductance Ca(2+)-activated K(+) channel in vascular smooth muscle: relationship between K(Ca) channel diversity and smooth muscle cell function	
REFERENCE	Circ. Res. (Online) 85 (9), E33-E43 (1999)	
AUTHORS	2 (bases 1 to 1899)	
TITLE	Neylon,C. and Reinhart,P.H.	
JOURNAL	Direct Submission	
FEATURES	Submitted (27-Sep-1999) Neurobiology, Duke University Medical Center, Research Drive, Durham, NC 27514, USA	
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Page 21

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Tue May 15 08:41:20 2001

us-09-254-590-19.rge

Page 22

Tue May 15 08:41:35 2001

us-09-254-590-21.rst

Page 1

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

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110: em_esthum76:*
111: em_esthum77:*
112: em_esthum78:*
113: em_esthum79:*
114: em_esthum80:*
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116: em_esthum82:*

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 189: gb_est120.*

190: em_gss_pin1.*
 191: em_gss_pin2.*
 192: em_gss_pro.*
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 194: em_gss_rod2.*
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 197: em_gss_rod5.*
 198: em_gss_vrt1.*
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 229: em_gss_vrt32.*
 230: em_gss_vrt33.*
 231: em_gss_vrt34.*
 232: em_gss_vrt35.*
 233: em_gss_vrt36.*
 234: em_gss_vrt37.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Query Length	ID	Description
1	741.8	42.6	754	138	BE671791
2	593.4	34.1	635	148	BE527328
3	521.2	30.0	562	148	BF436970
4	468.8	26.9	521	118	AM659534
5	466	26.8	538	139	BE750923
6	461.2	26.5	538	139	BE751606
7	450	25.9	475	102	AI810558
8	408	23.4	689	115	AM411311
9	393.2	22.6	437	213	AO937061
10	364	20.9	847	165	BE276011
11	362	20.8	714	165	BE297121
12	345.8	19.9	827	146	BE306047
13	317	18.2	405	21	AI509203
14	317	18.2	410	4	AA288411
15	315.6	18.1	731	166	BE397619
16	311.6	18.0	476	3	AA209646
17	311.6	17.9	474	4	AA238176
18	279.2	16.0	875	136	BE562092

19	249.4	14.3	887	107	AU118918	AU118918	AU118918
20	246.6	14.2	908	231	CNS0462N	AL291014	Tetradon
21	238	13.7	526	136	BE513322	BE513322	601315512
22	229.6	13.2	260	147	BE372874	BE372874	MR0-FT008
23	229.6	13.2	544	148	BE437112	BE437112	7P63612.x
24	226.8	13.0	250	147	BE372882	BE372882	MR0-FT008
25	220	12.6	451	137	BE655976	BE655976	UI-M-BH0
26	217.6	12.5	537	150	BE550943	BE550943	UI-R-C1-k
27	217.4	12.5	474	7	AA418096	AA418096	zy94b01.r
28	216.8	12.5	985	231	CNS0462N	AL273440	Tetradon
29	213.8	12.3	987	229	CNS0150D	AL163478	Tetradon
30	203.6	11.7	872	141	BE890992	BE890992	601431984
31	202.8	11.7	535	23	AI671578	AI671578	wb33h06.x
32	198	11.4	203	138	BE704259	BE704259	MR3-NN112
33	193.8	11.1	1020	230	CNS020LH	AL206646	Tetradon
34	190.2	10.9	525	150	BF562969	BF562969	UI-R-B00-
35	189.6	10.9	591	122	AW68762	AW68762	ESTR80838
36	184.4	10.6	251	160	BR580461	BR580461	BR580461
37	184.2	10.6	419	11	AA767647	AA767647	oa91E12.s
38	176	10.1	478	11	AA731772	AA731772	nb54h05.s
39	173.4	10.0	534	23	AI669070	AI669070	HB84a05.x
40	171.8	9.9	278	152	F11363	F11363	HSC2VH041n
41	171.8	9.9	323	114	AB381734	AB381734	QV1-HT031
42	171.8	9.9	324	114	AB381738	AB381738	QV1-HT031
43	170.8	9.8	341	173	BE084391	BE084391	H3100C10-
44	161.8	9.3	722	151	BE684857	BE684857	602142572
45	160.6	9.2	336	163	BE151937	BE151937	QV1-HT031

ALIGNMENTS

RESULT 1
 LOCUS BE671791 754 bp mRNA EST 08-SEP-2000
 DEFINITION 7a45d10.x1 NCI-CGAP-GC6 Homo sapiens cDNA clone IMAGE:3221683
 RSK2.1, mRNA sequence.

ACCESSION BE671791
 VERSION BE671791.1 GI:10032332
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 754)
 AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
 TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 JOURNAL Unpublished (1997)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Tel: (301) 496-1550
 Email: Robert.Strausberg@nih.gov
 Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael
 R. Emmert-Buck, M.D., Ph.D.
 cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
 Bonaldo, Ph.D.
 cDNA Library Arrayed by: Greg Lennon, Ph.D.
 DNA Sequencing by: Washington University Genome Sequencing Center
 Clone distribution: NCI-CGAP clone distribution information can be
 found through the I.M.A.G.E. Consortium/ILN/ILN, send email to:
 info@image.llnl.gov
 Seq primer: -400P from Gibco
 High quality sequence stop: 482.
 Location/Qualifiers

FEATURES
 SOURCE
 1..754
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:3221683"
 /clone_id="NCI-CGAP-GC6"
 /tissue_type="pooled germ cell tumors"
 /lab_host="DH10B"
 /note="Vector: pT73D-Pac (Pharmacia) with a modified

polylinker: Plasmid DNA from the normalized library
 NCI-CGAP-GC4 was prepared, and ss circles were made in
 vitro. Following HAP purification, this DNA was used as
 tracer in a subtractive hybridization reaction. The driver
 was PCR-amplified cDNAs from a pool of 5,000 clones made
 from the same library (clones 1257096-1258631,
 1469064-1470983, and 147592-1476743). Subtraction by
 Bento Soares and M. Fatima Bonaldo.
 1 others

BASE COUNT	157 a	232 c	213 g	151 t
ORIGIN				
Query Match	42.6%	Score 741.8:	DB 138:	Length 754:
Best Local Similarity	98.9%	Pred. No 9.7e-184:		
Matches 746:	Conservative	0: Mismatches	8: Indels	0: Gaps
33	CGGCGCGTACACAACTTGAGCCGCTCCCGGACACTTCACAGATGAGTACAGAGC	92		
1	GGGCGCGTACACAACTTGAGCCGCTCCCGGACACTTCACAGATGAGTACAGAGC	60		
93	GCAAGCCCTGACAGCCCGGCTGTCGAGAGAGTGGCGGCTCCCTCCGCTGTC	152		
61	GCAGCCCTGACAGCCCGGCTGTCGAGAGAGTGGCGGCTCCCTCCGCTGTC	120		
153	AGCGCTGCGCGCGCGCGCTGTTCTGCTCAGCCCGGAGATGCTGTTAAACC	212		
121	AGCGCTGCGCGCGCGCGCTGTTCTGCTCAGCCCGGAGATGCTGTTAAACC	180		
213	CGAGCAGACACTCCACAACTGCGCTCTATGAAACCGCGCGGAGAGAGAGC	272		
181	CGAGCAGACACTCCACAACTGCGCTCTATGAAACCGCGCGGAGAGAGAGC	240		
273	AGGAGCGCGCGCGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	332		
241	AGGAGCGCGCGCGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	300		
333	AAAGAAAAACAGAACTGCGCTGACAGCTGGCGGCGCGGCGGCGGCGGCGG	392		
301	AAAGAAAAACAGAACTGCGCTGACAGCTGGCGGCGGCGGCGGCGGCGGCGG	360		
393	CAAGCGCGTACAGCTGACAGCTGATCTGCGGATGCGGATGCGGATGCGGAT	452		
361	CAAGCGCGTACAGCTGACAGCTGATCTGCGGATGCGGATGCGGATGCGGAT	420		
453	CGAGACCGAGCTGCTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG	512		
421	CGAGACCGAGCTGCTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG	480		
513	ATGCTTATCAGTCTCCACAGATCCTGCTGCTGATGATGCTGATGATGATG	572		
481	ATGCTTATCAGTCTCCACAGATCCTGCTGCTGATGATGCTGATGATGATG	540		
573	GGAATATACATGTCATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	632		
541	GGAATATACATGTCATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	600		
601	TGAGCGATTTCTTCTATCTGCTGGAATATCTGCTGCTGCTGCTGCTGCTG	660		
633	TGAGCGATTTCTTCTATCTGCTGGAATATCTGCTGCTGCTGCTGCTGCTG	692		
693	GATATATCATTCATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	752		
661	GATATATCATTCATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	720		
753	CGCTGATGATGATTTTATCTATACCAATG	786		
721	CGCTGATGATGATTTTATCTATACCAATG	754		

RESULT 2
 LOCUS BE527328 635 bp mRNA EST 11-DEC-2000
 DEFINITION 602039710P2 NCI-CGAP-Brn67 Homo sapiens cDNA clone IMAGE:4177467

Thu May 15 08:41:35 2001

us-09-254-590-21.rst

Page 4

ACCESSION 5', mRNA sequence.
VERSION BF527328
KEYWORDS EST.
SOURCE Human.
ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
AUTHORS 1 (bases 1 to 635)
TITLE NIH-MGC http://mgs.nci.nih.gov/
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert.L.Strausberg@nih.gov

Issue Procurement: David N. Louis, M.D.
CDNA Library Preparation: Life Technologies, Inc.
DNA Sequencing by: InCyte Genomics, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
Found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov
Plate: L1M9484 row: c column: 04
High quality sequence stop: 631.
Location/Qualifiers

FEATURES
SOURCE 1. 635
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4177467"
/clone_lib="NCI_CGAP_Pr28"
/tissue_type="anaplastic oligodendroglioma with 1p/19q
loss"
/lab_host="DH10B (T1 phage-resistant)"
/note="Organ: brain; Vector: pCMV-Sport6; Site: 1; Note:
Site: 2; Salt: Cloned unidirectionally. Primer: Oligo dT.
Average insert size 2.3 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."

BASE COUNT 156 a 155 c 139 g 185 t
ORIGIN

Query Match 34.1%; Score 593.4; DB 149; Length 635;
Best Local Similarity 99.2%; Pred. No. 8.1e-145;
Matches 628; Conservative 0; Mismatches 1; Indels 4; Gaps 3;
QY 385 GAAAGGCGAAGGCGCTCAGGACTACGCGCTCATCTTCGCGATGTCGGCATCTGCTC
DB 1 GAAAGGCGAAGGCGCTCAGGACTACGCGCTCATCTTCGCGATGTCGGCATCTGCTC
QY 445 ATGCTCATCGAGACCGAGCTGCTGCGGCGCTCAGCAAGCGCTGCTGATTCCTTA
DB 61 ATGCTCATCGAGACCGAGCTGCTGCGGCGCTCAGCAAGCGCTGCTGATTCCTTA
QY 505 GCTCTGAATGCTTATCATCTCTCAGCATATCTGCTCGTGTATCATGCTGATTC
DB 121 GCTCTGAATGCTTATCATCTCTCAGCATATCTGCTCGTGTATCATGCTGATTC
QY 565 CAGCGAGGAAATACAGTGTTCATGCTGACATGAGCAAGATGACTGAGAAATAGCC
DB 181 CAGCGCA-GGAAATACAGTGTTCATGCTGACATGAGCAAGATGACTGAGAAATAGCC
QY 625 ATGACTTATGAGCGTATTTCTTCATCGCTGGAATATCTGCTGCTATTCATTCGCC
DB 240 ATGACTTATGAGCGTATTTCTTCATCGCTGGAATATCTGCTGCTATTCATTCGCC
QY 685 ATACCTGGAAATATACATTCACATGACGCGCGCTGCTGCTATTCATTCGCC
DB 300 ATACCTGGAAATATACATTCACATGACGCGCGCTGCTGCTATTCATTCGCC
QY 745 ACAACGACGCTGATGATATATTTATCATACCAATGCTTAAAGACTATATCTG
DB 360 ACAACGACGCTGATGATATATTTATCATACCAATGCTTAAAGACTATATCTG

QY 805 ATGCGACGATGATGCTTTTACATAGCAAACTTTTACATGATGCTCTCTAGACCAT
DB 420 ATGCGACGATGATGCTTTTACATAGCAAACTTTTACATGATGCTCTCTAGACCAT
QY 865 GAGCAGCTTATATAGATTAATCAATCAATGCTTTGTTATGACCTTTAATGACTATA
DB 480 GAGCAGCTTATATAGATTAATCAATCAATGCTTTGTTATGACCTTTAATGACTATA
QY 925 TCCGAGGAGCTGATCTGCTGTTTATGATTCATTAATGATTAATGCGGAGGACT
DB 540 TCCGAGGAGCTGATCTGCTGTTTATGATTCATTAATGATTAATGCGGAGGACT
QY 985 GTCCGAGCTGTTGAAA-GGTACCATGATCAAC 1015
DB 599 GTCCGAGCTGTTGAAA-GGTACCATGATCAAC 631

RESULT 3
BF436970 562 bp mRNA EST 29-NOV-2000
LOCUS BF436970
DEFINITION similar to TR:P70604 P70604 CALCIUM-ACTIVATED POTASSIUM CHANNEL
sequence.
ACCESSION BF436970
VERSION BF436970.1 GI:11449288
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
AUTHORS 1 (bases 1 to 562)
TITLE NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
JOURNAL National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert.L.Strausberg@nih.gov

Tissue Procurement: Michael J. Brownstein, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
found through the I.M.A.G.E. Consortium/LNL, send email to:
InfoImage.llnl.gov
Seq primer: -400p from Gibco
High quality sequence stop: 500.
Location/Qualifiers
1. 562
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:3650936"
/clone_lib="NCI_CGAP_Pr28"
/sex="male"
/dev_stage="adult"
/lab_host="DH10B"
/note="Organ: prostate; Vector: pT73D-Pac (Pharmacia)
with a modified polylinker. Plasmid DNA from the
normalized library NCI_CGAP_Pr22 was prepared, and as
this DNA was used as tracer in a subtractive hybridization
reaction. The driver was PCR-amplified cDNAs from a pool
of 5,000 clones made from the same library (clonoids
985608-985759, 1101192-1101959, and 1217928-1220615).
Subtraction by Bento Soares and M. Fatima Bonaldo."

BASE COUNT 108 a 185 c 171 g 98 t
ORIGIN

Query Match 30.0%; Score 521.2; DB 148; Length 562;
Best Local Similarity 97.1%; Pred. No. 6.9e-126;

Matches 542; Conservative 0; Mismatches 13; Indels 3; Gaps 1;

47 ACTTGAGCGCTCCCGGCGGAGCTGACAGATGATCAGAGCGGAGCCCTGACG 106
 5 ACTTGAGCGCTCCCGGCGGAGCTGACAGATGATCAGAGCGGAGCCCTGACG 64
 107 CCCCCGCTGCTGAGAGAGTGGCGGCTCCCTCCCTGCTGACGCT---GCG 163
 65 CCCCCGCTGCTGAGAGAGTGGCGGCTCCCTCCCTGCTGACGCTGCGCG 124
 164 CCCCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 223
 125 CCCCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 184
 224 ACTCCACACACTGCGCTCTATGAAACGCGGCGGAGAGAGCTGAGAGCGGCG 283
 185 ACTCCACACACTGCGCTCTATGAAACGCGGCGGAGAGAGCTGAGAGCGGCG 244
 284 GCGGTGGCGGAGCGGCGGAGAGAGCTGAGAGAGCTGAGAGAGCTGAGAGAG 304
 245 GCGGTGGCGGAGCGGCGGAGAGAGCTGAGAGAGCTGAGAGAGCTGAGAGAG 304
 344 AGACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 403
 305 AGACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 364
 404 GCGACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 463
 365 GCGACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 424
 464 TGTGCTGGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 523
 425 TGTGCTGGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 484
 524 GTCCTCCACAGTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 583
 485 GTCCTCCACAGTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 544
 584 TGTTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 601
 545 TGTGCTGGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 562

RESULT 4
 AM659534 521 bp mRNA EST 14-JUL-2000
 LOCUS 96789 MARC 1BOV Bos taurus cDNA 5', mRNA sequence.
 DEFINITION AM659534
 ACCESSION AM659534.1 GI:7425361
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM Bos taurus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 Bovidae; Bovinae; Bos.
 1 (bases 1 to 521)
 Smith, T.P.L., Casas, E., Stone, R.T., Heaton, M.P., Grosse, W.M.,
 Bennett, G.A., Fahrenkrug, S.C., Freking, B.A., Rohrer, G.A., Laegreid
 W.M. and Keefe, J.W.
 Design and use of four pooled tissue normalized cDNA libraries for
 EST discovery in cattle
 Unpublished (2000)
 Contact: Smith TPL
 USDA, ARS US Meat Animal Research Center
 PO Box 166, Clay Center, NE 68933-0166, USA
 Tel: 402 762 4366
 Fax: 402 762 4390

JOURNAL
 COMMENT

Email: smithemail.marc.usda.gov
 Single pass sequencing. Bases called and alt. trimmed with phred
 v0.980904.e. Vector identified by cross-match with the -minscore 18
 and -mismatch 12 options.
 PCR Primers
 FORWARD: AGGAACAGTATGACCAT

BACKWARD: GTTTCACAGTACAGAG
 Plate: 74 row: J column: 10
 Seq primer: ATTGAGTGACATG.
 Location/Qualifiers

FEATURES
 source

1..521
 /organism="Bos taurus"
 /db_xref="taxon:9913"
 /clone_lib="MARC 1BOV"
 /tissue_type="pooled"
 /lab_host="DH10B"
 /note="Vector: pcMV SPORTE; Site 1: XbaI; Site 2: XhoI;
 library made from pooled tissue from lymph node, ovary,
 fat, hypothalamus, and pituitary."
 BASE COUNT 166 a 99 c 130 g 126 t
 ORIGIN

Query Match 26.9%; Score 468.8; DB 118; Length 521;
 Best Local Similarity 93.8%; Pred. No. 3.8e-112; Indels 0; Gaps 0;
 Matches 488; Conservative 0; Mismatches 32;

926 GCCCAGAGACTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 985
 2 GCCCAGAGACTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 61
 986 TCCGAGCTTGGAAGAGTACATGATGATGATGATGATGATGATGATGATGATGATGAT 121
 62 TCCGAGCTTGGAAGAGTACATGATGATGATGATGATGATGATGATGATGATGATGAT 121
 1046 TGTGCTGGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1105
 122 TGTGCTGGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 181
 1106 ACTGTGGAAGAGAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1165
 182 ATTGTGGAAGAGAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 241
 1166 TGTGCTGGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1225
 242 TGTGCTGGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 301
 1226 TCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1285
 302 TCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 361
 1286 AAACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1345
 362 AAACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 421
 1346 GAAACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1405
 422 GAAACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 481
 1406 AGAGGAACGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1445
 482 AGAGGAACGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 521

RESULT 5
 BE750923 538 bp mRNA EST 15-SEP-2000
 LOCUS 202596 MARC 2BOV Bos taurus cDNA 5', mRNA sequence.
 DEFINITION BE750923
 ACCESSION BE750923
 VERSION BE750923.1 GI:10164915
 KEYWORDS
 SOURCE
 ORGANISM Bos taurus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 Bovidae; Bovinae; Bos.
 1 (bases 1 to 538)
 Smith, T.P.L., Casas, E., Stone, R.T., Heaton, M.P., Grosse, W.M.,
 Bennett, G.A., Fahrenkrug, S.C., Freking, B.A., Rohrer, G.A., Laegreid

REFERENCE
 AUTHORS

REFERENCE
1 (bases 1 to 847)
Mammalia: Eutheria: Primates: Catarrhini: Homiidae: Homo.
AUTHORS
NIH-MGC <http://mgi.nci.nih.gov/>.
TITLE
National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL
Unpublished (1999)
CONTACT: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert.Strausberg@nih.gov

Tissue Procurement: ATCC/DC/DTP
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
DNA Distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: image.llnl.gov
Plate: LNCM136 row: 9 column: 01
High quality sequence start: 43
High quality sequence stop: 813.
Location/Qualifiers

FEATURES

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/db_xref="taxon:9606"
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/clone_lib="NIH_MGC_20"
/tissue_type="melanotic melanoma"
/lab_host="DH10B (phage-resistant)"
/note="Organ: skin; Vector: pOTB7; Site_1: XhoI; Site_2: EcoRI; CDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(5). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."
BASE COUNT 267 a 201 c 199 g 179 t 1 others
ORIGIN

Query Match 20.9%; Score 364; DB 165; Length 847;
Best Local Similarity 96.9%; Pred. No. 1.4e-84;
Matches 403; Conservative 0; Mismatches 10; Indels 3; Gaps 3;

QY 1002 GTACCATGATCAGACAGAGTGTACTAGCACTCTCTGGAGCGATGGTGTATATCAAT 1061
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Db 429 GTACCATGATCAGACAGAGTGTACTAGCACTCTCTGGAGCGATGGTGTATATCAAT 488
QY 1062 AACCTTCTCATTGTTTANGTGACATGATGATCAACATCTGTGAAAGAGT 1121
|||||
Db 489 AACCTTCTCATTGTTTANGTGACATGATGATCAACATCTGTGAAAGAGT 547
QY 1122 CTGCTTACTTACTGGAATATGAGTGCTGTGTCACAGCCCTGCTGATGCTAGTGGC 1181
|||||
Db 548 CTGCTTACTTACTGGAATATGAGTGCTGTGTCACAGCCCTGCTGATGCTAGTGGC 607
QY 1182 AAGGAAGTAACTTACCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 1241
|||||
Db 608 AAGGAAGTAACTTACCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 667
QY 1242 GCTGACTAAAGAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAA 1301
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Db 668 GCTGACTAAAGAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAA 726
QY 1302 CAATAATACAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAA 1361
|||||
Db 727 CAATAATACAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAA 785
QY 1362 ATCTCTGCAAGCTATTCATTAAGAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAG 1417
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Db 786 ATCTCTGCAAGCTATTCATTAAGAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAA 841

RESULT 11
BE297121 714 bp mRNA EST 20-JUL-2000
LOCUS BE297121 714 bp mRNA EST 20-JUL-2000

DEFINITION
601177509F1 NIH_MGC_17 Homo sapiens CDNA clone IMAGE:3532683 5',
mRNA sequence.
ACCESSION
BE297121
VERSION
BE297121.1
KEYWORDS
EST.
SOURCE
human.
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE
1 (bases 1 to 714)
NIH-MGC <http://mgi.nci.nih.gov/>.
TITLE
National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL
Unpublished (1999)
CONTACT: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert.Strausberg@nih.gov

Tissue Procurement: ATCC
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
DNA Distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: image.llnl.gov
Plate: LNCM209 row: a column: 04
High quality sequence stop: 613.
Location/Qualifiers

FEATURES

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/tissue_type="rhabdomyosarcoma"
/lab_host="DH10B (phage-resistant)"
/note="Organ: muscle; Vector: pOTB7; Site_1: EcoRI; Site_2: XhoI; CDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(5). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."
BASE COUNT 126 a 226 c 178 g 184 t
ORIGIN

Query Match 20.8%; Score 362; DB 165; Length 714;
Best Local Similarity 71.0%; Pred. No. 4.4e-84;
Matches 507; Conservative 0; Mismatches 205; Indels 2; Gaps 2;

QY 448 GTTCATCGAGACGAGCTGCTGAGGCGCCTACGACAGGCGCTGATTCCTTACT 507
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Db 1 GTTCATCGAGACGAGCTGCTGAGGCGCCTACGACAGGCGCTGATTCCTTACT 507
QY 508 CTGAAATGCTTATACATGCTCTGACATCATCTCTTGTGGCTTATATGCGCTACAC 120
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Db 61 CTGAAATGCTTATACATGCTCTGACATCATCTCTTGTGGCTTATATGCGCTACAC 120
QY 568 GCCAGGGAATACAGTTTTCATGTTGATGAGCAAGGAGATGAGTACGAGATAGCCATG 627
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Db 121 ACAGGTGAAGTCCAGCTCTTGTGATGAGCAAGGAGATGAGTACGAGATAGCCATG 180
QY 628 ACTTATGAGCTATTTCTTATCTCTGATGAGTAAATATGTTGTTGATGATGATGATG 687
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Db 181 ACTTATGAGCTATTTCTTATCTCTGATGAGTAAATATGTTGTTGATGATGATGATG 240
QY 688 CTGAGGATTAATACATGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 747
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Db 241 CTGAGGATTAATACATGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 300
QY 748 ACCACCGCTGATGAGTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTT 807
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Db 301 GCGAGGCGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 360
QY 808 GCGAGGCGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 867

US-09-254-590-21.rst

Db	361	GCCTGATATCTCTGACACACCAAGCTTCCAGATGCCGATTCCTGCTCCGACACATCCGG	420
Oy	868	GCACCTTAATAGATAAATCTCAATACAGCTTTGGTTATATGAAGACTTTAATGACTATATGC	927
Db	421	GCCCTCAACAAAGATCAATTCACACCCGCTTTGTATGATGAAGAGCTCAATGACATCTGC	480
Oy	928	CCAGAGACTACTCTTGGTTTTTATGATCTCAATTATGAGTAATTTGCCATGAGCATGTC	987
Db	481	CTGAGCATGTGCTGCTGCTGTTCAGCATCTCTCTGTGAACTATCTCCTCGAGACGTC	540
Oy	988	CGAGCTTGTGAAGAGACCAATGATCAACAGATGTTACTAGCAACTCTCTTGGAGCAT	1047
Db	541	CGTGTCTGTGAAGTAGACCATACACACAGACAGCG-TACTAGTAACCTTCTGGGTGCATG	599
Oy	1048	TGGTTGATATCATTAATCTTCTCTCCATTTGGTTATGATGAAGTATACCTTAACATACAC	1107
Db	600	TGGCTCATCTCATCTCATCTCTCTTCT-TTGGTATAGGGGAGCTGTGCCCCCCCATATCTG	658
Oy	1108	TGTGAAGAAGAGCTGCTTACTTATCTGAATTTATGGGTCTGGTTTGGACAGCC	1161
Db	659	TGGAGAGTCTCTCCCTCAACGGCTCTGGTGTGGCTGTGGCTGTTTGGTGTGCC	712

RESULT	12
BF306047	
LOCUS	827 bp
DEFINITION	mRNA
ACCESION	60189375611 NIH_MGC_17 Homo sapiens CDNA clone IMAGE:4139388 5'
VERSION	BF306047
KEYWORDS	BF306047.1 GI:11253116
SOURCE	EST.
	human.

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

(ibaes 1 to 827)
PIMARES; Catarrhini; Homidae; Homo.
NIH-MGC <http://mgc.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999).
Contact: Robert Struelens@nci.nih.gov

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High quality sequence stop: 731.
location/Qual/Ref
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/lab_host="DH10b (phage-resistant)"
/note="Organ: muscle; Vector: pCMV7; Site_1: EcoRI;
Site_2: XhoI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCACGAG(G). Size-selected >500bp
for average insert size 1.8kb. Library constructed by
ling Hong in the laboratory of Gerald M. Rubin (University
of California, Berkeley) using zap-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."

BASE COUNT 159 a 247 c 223 g 198 t

Query Match	19.9%;	Score 345.8;	DB 146;	Length 827,
Best Local Similarity	73.3%;	Pred. No. 8.1e-80;		

Matches 496; Conservative 0; Mismatches 177; Indels 4; Gaps 4,
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Db 130 TTTTGTGGCCCTGAAATAGCTCTTATCGTCTCTCCACCATCATCTCT-TGGGCTGATGAT 557

Qy 558 CGTGTACCAACGGCAGAGGAAATACAGTGTGTATGTGTGACAAATGGACAGATAGCTAGAG 617

Db 189 CGCGTCAACACAGCTGAAGTCCAGCTCTTCTGTGATCGACAACCGCCGAGATGACTGGCG 248

Qy 618 AATAGCAATGACCTATATAGCGTATTTCTTCATCTGCTTGGAAATACGTGTGTGCGTAT 677

Db 249 GATAGCGATGACCTACAGACGGGATCTCTCATCATCAGCTGGAGATCTGTGTGCCCAT 111

Qy 678 TCATCCCATACCTGGGAAATTATACATTCACATGAGAGGCCCGGCTGCTTCTCTATGC 737

Db 309 CCACCCCTTCTCTGGCGAGTCAAGATTCTCTTGAGAGCGACAGCTGGCTCTCTCTACAC 368

Qy 738 CCCATCCACAACACACCGCTGATGTGGATATATTATATCTATACAAATGTTCTTAAGACT 797

Db 369 ACCCTCCGGGGGAGAGCCGATGTGGACATCTCTGTATCCCAATGTTCTTGCGCT 428

Qy 798 CTATGTGATTCGCAGAGTCATGCTTTTACATAGCAAACTTTCACGATGCGTCCCTG 857

Db 429 GTACCTATATGCCCCAGATCATGCTGCTGCACAGCAACTCTTCCAGATGCTCTGTCGG 488

Qy 858 AAGCATTTGAGACACTTAATAGATTAACCTCAATACAGCTTTTGTATGAAGACTTTAT 917

Db 489 CAGATGGGGGC-CTCAACAAGATCAACTCAACACCCCTTGTGATGAAGACGTCAT 547

Qy 918 GACTATATGCCAGGAACTGATCTCTGTTTTAGTATCTCATTAATGATTAATGGCG 977

Db 548 GACCATCTG-CTGSCACTGTGCTGCTGTGTTACAACTCTCTGTGATCAATTGTGC 606

Qy 978 ATGACATGTCGCACTGTGTGAAGGTACATGATCAACAGATGTTACTAGCAACTTCT 1037

Db 607 CTGGACCGTCCGTTCTGTGTAAAGGTACATGACACGACAGCACTAATGTAACCTTTC 666

Qy 1038 TGGAGCGATGTGGTTGATATCAATACCTTTCTCTCAATGGTTATGTGACATGTGACC 1097

Db 667 TGGGTGGGATGTGTCATCTCCATCAATTCCTTTTCATTTGTTATGGGACATGGGTGC 726

Qy 1098 TAACACATACTGTGAAAGAGAGTCTCTTACTACTCTGAAATTAATGGTCTGGTTGCAC 1157

Db 727 CCACACATACTGTGGAAAGAGTCTCTCTCTCACTGG-ATTCAAGGTGCAAGGTTGCAT 785

Qy 1158 AGCCCTGGTGTAGCTG 1174

Db 786 TGGCCCTGTGTGGCG 802

RESULT 13
LOCUS AI509203
DEFINITION AI509203 405 bp mRNA EST 12-MAR-1999
vbl4ed4.y1 Soares mouse NML Mus musculus cDNA clone IMAGE:748734 5
similar to tr:P70604 P70604 CALCIUM-ACTIVATED POTASSIUM CHANNEL
RS2.1, mRNA sequence.
ACCESSION AI509203
VERSION AI509203.1 GI:4408108
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Mammalia; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Euteleostei; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 405)
AUTHORS Marra,M., Hillier,B., Kucaba,T., Marlin,J., Beck,C., Wylie,T.,
Underwood,K., Stepien,M., Theising,B., Allen,M., Bowers,Y., Person
,B., Swallier,T., Gibbons,M., Pape,D., Harrey,N., Schurk,R., Rittler
,E., Kohn,S., Shih,T., Jackson,Y., Cardenas,M., McCann,R.,
Katerstein,R. and Wilson,R.
TITLE The WashU-NCI Mouse EST Project 1999
JOURNAL Unpublished (1999)
CONTACT: Marra M/WashU-NCI Mouse EST Project 1999

Tue May 15 08:41:35 2001

us-09-254-590-21.rst

Page 12

Db 301 GCGTCCCGGTCCTGTCACAGAGCGGCGTCTCTCCACAGCGCCACCAATTTCATC 360
QY 1728 AGAGAGTACTAG 1740
Db 361 AGAGAGTACTAG 373

RESULT 15
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LOCUS BE397619 731 bp mRNA EST 21-JUL-2000
DEFINITION 601289422P1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3620014 5',
RNA sequence.
ACCESSION BE397619
VERSION BE397619.1 GI:9342984
KEYWORDS EST.
SOURCE human.

ORGANISM

Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
NIH-MGC http://mgs.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1998)
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert.Strausberg@nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
cDNA Library Preparation: Ling Hong/Rubin Laboratory
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LMNL)
Cloning distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LMNL at: image.lmnl.gov
High quality sequence start: 3
High quality sequence stop: 662.
Location/Qualifiers
1. 731

FEATURES
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/clone="IMAGE:3620014"
/clone_lib="NIH_MGC_8"
/tissue_type="Burkitt lymphoma"
/lab_host="DH10B (phage-resistant)"
/note="Organ: Lymph. Vector: pOT87; Site:1: XhoI; Site:2:
EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGCAGCAG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."
BASE COUNT 142 a 220 c 187 g 182 t
ORIGIN

Query Match

Best Local Similarity 18.1%; Score 315.6; DB 166; Length 731;
Matches 411; Conservative 0; Mismatches 139; Indels 2; Gaps 1;

QY 484 AAGCGTCGCTATTCCTTACGTCGAATGCTTATCAGTCTCCACGATCATCTG 543
Db 170 AAGGACTCCATTTTCCTGCGCCGTAATGCTTATCAGTCTCCACGATCATCTT 229
QY 544 CTGGGTCGATATCGTGTCACAGCGCGAATATACAGTGTTCATGGTGAGCAATGCA 603
Db 230 TTGGGCTTATATCGCTACACACAGTGAAGTCCAGCTCTTCGATGACCAATGCG 289
QY 604 GCAGATGACTGAGATAGCAGTATGAGGCTATTTCTCATCTGCTTGAATA 663
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QY 664 CTGGTGTGCTATTCATCCATACCTGGGATTTATATTCATGAGCGCGCGCTT 723

Db 350 CTGATGCGGCGATCAGACCCATCTCTGCGAGTACAGTTCCTTGGACGCGACGCTT 409
QY 724 GCGTCTCTATGCCCCATCCACACACACCGCTGATGATATTTATTTATATACCA 783
Db 410 GCGTCTCTATGCCCCATCCACACACCGCTGATGATATTTATTTATATACCA 783
QY 784 ATGTTCTTAAGACTCTATCTGATGATGCGAGTCAATGCTTTACATAGCAACTTTTACT 843
Db 470 ATGTTCTGCGCCCTGATGATGCGAGTCAATGCTTTACATAGCAACTTTTACT 843
QY 844 GATGCTCTCTAGAGCAATGAGACACTTATATAGATTAACCTCAATACAGCTTTTGT 903
Db 530 GATGCTCTCTAGAGCAATGAGACACTTATATAGATTAACCTCAATACAGCTTTTGT 903
QY 904 ATGAGACTTTATATGATATATGCGAGAACTGATCTTGTGTTTACTATCTCATTA 963
Db 590 ATGAGAGCGCTCATGACATGCTGCGGACATGCTGCTGCTGCTGCTGCTGCTGCTG 649
QY 964 TGGATTAATGCGCGATGAGTCTGCGAGCTTGGAAAGTACATGATCAAGAGATGT 1023
Db 650 TGGATTAATGCGCGATGAGTCTGCGAGCTTGGAAAGTACATGATCAAGAGATGT 1023
QY 1024 ACTAGCAACTTC 1035
Db 708 ACTAGTACTTC 719

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Job time: 8901 sec

Tue May 15 08:41:35 2001

us-09-254-590-21.rst

True May 15 08:41:21 2001

us-09-254-590-19.rng

OM of: US-09-254-590-19 to: N_Geneseq_0401.* out_format: pfs
Date: May 14, 2001 11:03 PM

About: Results were produced by the Gencore software, version 4.5,
Copyright (c) 1993-2000 CompuGen Ltd.

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-DELOP=6.000 -DELEXT=7.000 -STRAT=1 -MATRIX=blomsub2
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Search information block:

Query: US-09-254-590-19
Query length: 579
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XX: V35457;
XX: 01-OCT-1998 (first entry)
XX: Human hSK2 coding sequence.
XX: Small conductance calcium-activated potassium channel protein 2;
XX: hSK2; human; potassium ion flux; ss.
XX: Homo sapiens.
XX: W0981139-A1.
XX: 19-MAR-1998.
XX: 10-SEP-1997; 97MO-US16033.
XX: 17-APR-1997; 97US-0045233.
XX: 11-SEP-1996; 96US-0026451.
XX: 07-MAR-1997; 97US-0040052.
XX: (ICAG-) ICAGEN INC.
XX: (UYOR-) UNIV OREGON HEALTH SCI.
XX: Adelman JP, Bond CT, Maylie J, Silvia CP;
XX: WPI: 1998-207332/18.
XX: P-PSDB: W63707.
XX: DNA encoding calcium-activated potassium channel - useful in assays
XX: to identify compounds which increase or decrease potassium ion flux
XX: Claim 3; Page 110-111; 151pp; English.

This sequence encodes the human small conductance calcium-activated potassium channel protein 2 (hSK2) of the invention. The proteins of the invention are monomers of a calcium-activated potassium channel, where the monomer: (i) has a calculated molecular weight of between 40 and 80 kDa; and (ii) has a unit conductance of between 2 and 60 pS when the monomer is in a Xenopus oocyte. Antibodies specific for the protein, and expressed in a Xenopus oocyte. Antibodies specific for the presence of the protein specific for the DNA can be used to detect the presence of the protein or DNA sequences in a sample. Host cells expressing the host protein can be used in assays to identify compounds which increase or decrease the potassium ion flux through the protein. The protein. The cell can also be used for the recombinant production of the protein. The DNA sequences can also be used for determine mutations in the SK and IK genes genes in a computer system. The proteins encoded by the SK and IK genes can be used in a computer system for determining their three dimensional structure, which is useful for determining ligands that bind to the proteins.

Sequence 1740 BP; 473 A; 432 C; 435 G; 400 T; 0 other:
SQ
alignment_scores: Length: 579
Quality: 2954.00
Ratio: 5.102
Percent Similarity: 100.000
Percent Identity: 100.000
Gaps: 0
alignment_block:
US-09-254-590-19 x V35457

Tue May 15 08:41:21 2001

us-09-254-590-19.rng

Page 2

Align seg 1/1 to: V35457 from: 1 to: 1740

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1 MetSerSerCysArgTyrAsnGlyValMetArgProLeuSerAsnLe 17
1 ATGAGCAGCTGCAGGTACAAAGGGGGCTGATGCGCGCTCAGCAACT 50
17 userAlaSerArgArgAsnLeuHisGluMetAspSerGluAlaInProL 34
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34 euGlnProProAlaSerValGlyGlyGlyGlyGlyGlyGlyGlyGly 50
101 TCGACCCCGCGCTGCTGCGAGAGAGGTGCGCGCTGCTCCCGCT 150
51 AlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAla 67
151 GCGAGCGCGCGCGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCT 200
67 lvalSerLysProGluHisAsnAsnSerAsnAsnLeuAlaLeuTyrGly 84
201 GGTGCTTAAGCCCGAGACAACTCAAACTGCGCGCTGCTGCTGCT 250
84 hrgLysGlyGlyGlySerThrGlyGlyGlyGlyGlyGlyGlyGlyGly 100
251 CCGCGCGCGAGCGAGCAGTGAAGAGCGCGCGCGCGCGCGCGCG 300
101 HisGlySerSerSerGlyThrLysSerSerLysLysAsnGlnAsn 117
301 CACGCGAGCAGAGTGCACCAAGTCCAGCAAAAGAAACCAAGACAT 350
117 eGlyTyrLysLeuGlyHisArgArgAlaLeuPheGlyLysArgLysArg 134
351 CGGCTACAAAGCTGGGCGCGCGCGCGCGCTGCTGCAAAAGCCAGCG 400
134 euSerAspTyrAlaLeuLeuLeuPheGlyMetPheGlyLeuVal 150
401 TCGAGCTACGCGCTCATCTTGGCATGTTGCGCATGCTGCTGCTGCT 450
151 lIeGluThrGluLeuSerTrpGlyAlaTyrAspLysAlaSerLeuTyr 167
451 ATCGAGACGAGCTGCTGCGCGCGCGCTGCAAGCAAGCGCTGCTGCT 500
167 rLeuAlaLeuLysCysLeuLysLeuSerThrLysLeuLeuGly 184
501 CTGAGCTGCAAAATGCTTATCATGCTCTCCAGCATCATCTGCTGCT 550
184 euLeuLeuValTyrHisAlaArgGluLeuGluPheMetValAspAsn 200
551 TGAATCATGCTGACCGAGCGCAAGGAATGATGCTGCTGCTGCTGCT 600
201 GlyAlaAspAspTrpArgIleAlaMetThrTyrGluArgLysPhePhe 217
601 GAGCAGATGACTGGAATAGCATGATGATGAGGATGATGCTGCTCAT 650
217 eCysLeuGluLeuValCysAlaLeuHisProLysProGlyAsnTyr 234
651 CTGCTTGGAAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 700
234 hPheThrTyrTrpThrAlaArgLeuAlaPheSerTyrAlaProSerThr 250
701 CATTCACATGAGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 750
251 ThrAlaAspValAspIleLeuSerLysProMetPheLeuArgLeu 267
751 ACCCGTGAATGATATATATATATATATATATATATATATATATAT 800
267 rLeuIleAlaArgValMetLeuLeuHisSerLysLeuPheThrAspAla 284
801 TCGATTCGCAAGATCATGCTTTCATGCAAACTTTTACATGAGTCT 850
284 eSerArgSerLysGlyAlaLeuAsnLysLysPheAsnThrArgPhe 300
|||||
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851 CCTGTAGAGCATTTGAGCACTTAATTAAGATTAATCTTCAATACGTTT 900
301 ValMetLysThrLeuMetThrLysCysProGlyThrValLeuLeuVal 317
901 GTTATGAAGACTTTAATGACTATATATGCGCAAGACTTACTGCTGCT 950
317 eSerLysLeuTrpIleLeuAlaAlaTrpThrValArgAlaCysGlu 334
951 TAGTATCTCATTTATGATTAATGCTGCTGCTGCTGCTGCTGCTGCT 1000
334 rGlyThrAspGlnGlnAspValThrSerAsnLeuGlyAlaMetTrp 350
1001 GGTACCATGATCAACAGAGTGTACTAGCAACTCTCTGAGGCAATG 1050
351 LeuLysSerLysThrPheLeuSerLysGlyTyrGlyAspMetValPro 367
1051 TTGATATCAATTAATCTTCTCTCATGTTGTTGTTGTTGTTGTTGTT 1100
367 nThrTyrCysGlyLysGlyValCysLeuLeuThrGlyLysMetGlyAla 384
1101 CACATCTGTGGAAGAGAGTCTCTTACTTACTGGAATATGCTGCTG 1150
384 LysThrAlaLeuValValAlaValAlaAlaArgLysLeuGluLeuThr 400
1151 GTTGACACCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 420
401 LysAlaGluLysHisValHisAsnPheMetLysThrGluLeuThr 417
1201 AAGCGAGAAACACGCGCAATTTTCAATGATGATGATGATGATGAT 1250
417 sArgValLysAsnAlaAlaAlaAsnValLeuArgLysLeuLeuLeu 434
1251 AAGAGTAAATAATGAGCTGCCAATGCTGCTGCTGCTGCTGCTGCT 1300
434 YrLysAsnThrLysLeuValLysLysLysLysLysLysLysLysLys 450
1301 ACAAAATACAAAGCTAGTGAAGAAAGATGATCATGCAAAAGTAAAG 1350
451 HisGlnArgLysPheLeuGlnAlaLeuHisGlnLeuArgSerVal 467
1351 CATCAACGAAATCTCTCAAGCTATTCATCATTAAGAAAGTAAAGT 1400
467 tGluGlnArgLysLeuAsnAspGlnAlaAsnThrLeuValAspLeuAla 484
1401 GGAACGAGAGAACTGAATACCAACCAACCACTTGTGCTGCTGCTG 1450
484 YrThrGlnAsnLysMetTyrAspMetLysSerAspLeuAsnGluArg 500
1451 AGACCGAGACATCATGATGATGATGATGATGATGATGATGATGAT 550
501 GluAspPheGlyLysArgLysValThrLeuGluThrLysLeuGluThr 517
1501 GAAGACTTTCGAGAGAGATTTGCTGCTGCTGCTGCTGCTGCTGCT 1550
517 uLysGlySerLysHisAlaLeuProGlyLeuLysGlnThrLysArg 534
1551 GATTGCTAGCATTCAGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1600
534 lGlnGlnArgAspPheIleGluAlaGluMetGluSerTyrAspLysHis 550
1601 AGCAGCAGAGAGATTTCAATGAGCTCATGAGAGCTGAGCTGAGCT 1650
551 ValThrTyrAsnAlaGluArgSerArgSerSerArgArgArgArg 567
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seq_documentation_block:
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ID V35446 standard; cDNA; 1740 BP.
 AC V35446;
 DT 01-Oct-1998 (first entry)
 DE Rat rSK2 coding sequence.
 XX Small conductance calcium-activated potassium channel protein 2;
 KW rSK2; rat; potassium ion flux; ss.
 XX Rattus sp.
 OS M0981139-A1.
 PN 19-MAR-1998.
 PD 10-SEP-1997; 97MO-US16033.
 PE 17-APR-1997; 97US-0045233.
 PR 11-SEP-1996; 96US-0026451.
 PR 07-MAR-1997; 97US-0040052.
 XX (ICAG-) ICAGEN INC.
 PA (UYOR-) UNIV OREGON HEALTH SCT.
 PI Adelman JP, Bond CT, Maylie J, Silvia CP;
 DR WPI: 1998-207332/18.
 DR P-PSDB; W63702.
 XX DNA encoding calcium-activated potassium channel - useful in assays
 PT to identify compounds which increase or decrease potassium ion flux
 PS Claim 3; Page 103-104; 151pp: English.
 XX This sequence encodes the rat small conductance calcium-activated
 CC potassium channel protein 2 (hSK2) of the invention. The proteins of the
 CC invention are monomers of a calcium-activated potassium channel, where
 CC the monomer: (i) has a calculated molecular weight of between 40 and
 CC 80 kDa; and (ii) has a unit conductance of between 2 and 60 pS when the
 CC monomer is in the functional polymeric form of a potassium chain and is
 CC expressed in a Xenopus oocyte. Antibodies specific for the protein, the
 CC probes specific for the DNA can be used to detect the presence of the
 CC protein or DNA sequences in a sample. Host cells expression of the
 CC protein can be used in assays to identify compounds which increase or
 CC decrease the potassium ion flux through the protein. The transfected host
 CC cell can also be used for the recombinant production of the protein. The
 CC DNA sequences can also be used for determine mutations in the SK and IK
 CC genes in a computer system. The proteins encoded by the SK and IK genes
 CC can be used in a computer system for determining their three dimensional
 CC structure, which is useful for determining ligands that bind to the
 CC proteins.
 SO Sequence 1740 BP; 467 A; 428 C; 442 G; 403 T; 0 other;

alignment_scores: Length: 584
 Quality: 2881.50 Gaps: 3
 Ratio: 5.020
 Percent Similarity: 98.288 Percent Identity: 97.603

alignment_block:

US-09-254-590-19 x V35446 ..

Align seg 1/1 to: V35446 from: 1 to: 1740

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 1 ATGAGCAGCTGCGAGTACAAAGGGGCGTCTGCGTCCGTGACCACTT 50
 17 userAlaSerArgArgAsnLeuHisGluMetAspSerGluAlaGlnProL 34
 |||

51 GAGCTGCTCCCGCCGGAACCTGCACAGATGAGACTCAGAGCTCAGCCCG 100
 34 euglinProProAlaSer...ValGlyGlyGlyGlyAlaSerSerPro 49
 101 TGCAGCCCGCCAGCGTGGTGTAGAGAGGAGTGGTGGTCTCTCCCG 150
 50 SerAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAla 66
 151 TCTGCTGCGCCCGCCCGCC.....TCATCTCCAGCCCGCAGAGAT 188
 66 eValAlaSerLysPProGluHisAsnAsnSerAsnAsnLeuAlaLeuTyrG 83
 189 CGTGGTGTCTAAGCCGAGCACACATTTCTAACAACTGGCGCTTACG 238
 83 LThrGlyGlyGlyGlySerThr.....GlyGlyGlyGlyGly 95
 239 GAACCTGGCGGCGGAGGAGCAGCCGAGGCGGCGGCGGCGGCGGCG 288
 96 GlyGlyGlySerGlyHisGlySerSerSerGlyThrLysSerSerLysLy 112
 289 GCGGCGGCGAGCGGCGCATGCGACAGCAGCGGCGCATAGTCCAGAAAA 338
 112 sLysAsnGlnAsnIleGlyTyrLysLeuGlyHisArgArgAlaLeuPheG 129
 339 GAAGAACACAGAACATCGCTATAGCTGGGCGCATCGGCGTGGCTTGG 388
 129 LulysArgLysArgLeuSerAspTyrAlaLeuIlePheGlyMetPheGly 145
 389 AGAAGCCCAAGCGGCTCAGCAGCTATGCGCTCATCTTGGAGTGTCCG 438
 146 IleValValMetValIleGluThrGluLeuSerTrpGlyAlaTyrAspLy 162
 439 ATCTGCTGATGCTCATGCTGACACCGACCTGCTGGGCGGCGTACAGAA 488
 162 sAlaSerLeuTyrSerLeuAlaLeuLysCysLeuIleSerLeuSerThrI 179
 489 GCGCTGCTGATTTCTTATGCTGTGAATGCTGTATGCTTCCACGA 538
 179 IleIleLeuLeuGlyLeuIleIleValIleValIleAlaArgGluIleGlu 195
 539 TCATCTGCTGCTGGTGTGATCATCATGATACACCGCCGGAATACACTTA 588
 196 PheMetValAspAsnGlyAlaAspAspTyrArgIleAlaMetThrTyrG 212
 589 TTCATGGTGCAAAATGAGCAGATGACATGGAATGACATGACTTATGA 638
 212 uArgIlePhePheIleCysLeuGluIleLeuValCysAlaIleHisProI 229
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 229 IeProGlyAsnTyrThrPheThrTyrThrAlaArgLeuAlaPheSerTyr 245
 689 TCCCTGGGAATATATGCTTCATGCAATGACAGCCCGGCTTGGCTTCTTAT 738
 246 AlaProSerThrThrThrAlaAspValAspIleIleLeuSerIleProMe 262
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 789 GTTCTTAAGACTATATGATGATGCAAGTCAAGTATTTATATGCAAAAC 838
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 889 TTCATATACGCTTTTGTATGAAGCTTTATATGATCATCTGCGCAGAAC 938
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329  aLaTgAlaCysGluArgTyrHisAspGlnGlnAspValThrSerAspPhe 345
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989  TCCGACCTGTGAAAGCTACCATGATCAACAGATGATCATTACCACTTC 1038
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346  LeuGlyAlaMetTyrPleuIleSerIleThrPheLeuSerIleGlyTyrG1 362
      |||
1039  CTTCGACCAATGCTGGTGAATCAATCAATCTTCTCCATTCGTTATGG 1088
      |||
362  yAspMetValProAsnThrTyrCysGlyLysGlyValCysLeuLeuThrG 379
      |||
1089  TGACATGCTACTACACATACACTGCGAAAGAGATCTCTGCTTACCG 1138
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379  LylleMeGlyAlaGlyCysThrAlaLeuValAlaValAlaValAlaArg 395
      |||
1139  GAATTAATGGGTGCAGTTGACAGCTTGGTGTACCGGTAGTGCAGAG 1188
      |||
396  LysLeuGluLeuThrLysAlaGlyLysHisValHisAspPheMetLys 412
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1189  AAGCTTACACTTACCAAAAGCAGAAAGCATGTGCATTTCTATGTA 1238
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412  pThrGlnLeuThrLysArgValLysAsnAlaAlaAsnValLeuArg 429
      |||
1239  TACTCAGCTGACCAAAAGATGAAAAAGCAGCCGCAATGTACTCAGG 1288
      |||
429  LuthrPleuIleTyrLysAsnThrLysLeuValLysLysIleAspHis 445
      |||
1289  AAGCTGTGTTAATCTACAAAAACACAAAGCTAGTGAAGAAAGATCCAC 1338
      |||
446  AlaLysValArgLysHisGlnArgLysPheLeuGlnAlaIleHisGlnLe 462
      |||
1339  GCMAAAGTAAAGAAAGCATACAGGAATTTCTTACAGCTTATTCATCA 1388
      |||
462  uArgSerValLysMetGlnArgLysLeuAsnAspGlnAlaAsnThrL 479
      |||
1389  AAGAGTGTGAACTGAACTGAAACAGAGAACTGAATGACCAAGCAATGCG 1438
      |||
479  euValAspLeuAlaLysThrGlnAsnIleMetLysPheMetIleSerAsp 495
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1439  TAGTGCATCTGCMAAGAACCCAGATATCATGTATGATATTCATTTCCGAC 1488
      |||
496  LeuAsnGluArgSerGluAspPheGluLysArgIleValThrLeuGluThr 512
      |||
1489  TTAATGTAAAGAGTGAAGACTTGAAGAAAGATGTCACCTGGAAGAC 1538
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512  LysLeuGluThrLeuIleGlySerIleHisAlaLeuProGlyLeuIleS 529
      |||
1539  AAAATTAGAAGCTTGTGATGTGATCATTCCTCCCTCGGCTTATCA 1588
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529  erGlnThrIleArgGlnGlnArgAspPheIleGluAlaGlnMetGlu 545
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1589  GCCAGACCATCAGACAGCAGCAAGGAGCTTCATGAGACACAGATGAG 1638
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546  SerTyrAspLysHisValThrTyrAsnAlaGluArgSerArgSerSer 562
      |||
1639  AACCTATGACAAAGCATGTACATCAATCAATGCTAGCGTCCCTCCCTC 1688
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562  rArgArgArgArgSerSerSerThrAlaProProThrSerSerGlnSer 579
      |||
1689  CAGGAGCGCGGCTCTCTCCACAGCGCCACCAACTCATCTGAGTA 1738
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1739  GC 1740

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ID V35458 standard: cDNA, 1674 bp.
AC V35458:
XX
XX
DT 01-OCT-1998 (first entry)

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XX
DE Truncated human hSK3 coding sequence.
XX
KW Small conductance calcium-activated potassium channel protein 3;
XX hSK3; human; potassium ion flux; ss.
XX
OS Homo sapiens.
XX
PN W09811139-A1.
XX
PD 19-MAR-1998.
XX
PF 10-SEP-1997; 97MO-US16033.
XX
PR 17-APR-1997; 97US-0045233.
XX
PR 11-SEP-1996; 96US-0026451.
XX
PR 07-MAR-1997; 97US-0040052.
XX
PA (ICAG-) ICAGEN INC.
XX (UOR-) UNIV OREGON HEALTH SCI.
XX
PA Adelman JP, Bond CT, Maylie J, Silvia CP;
XX
DR WPI: 1998-207332/18.
XX
DR P-PSDB: W63708.
XX
PT DNA encoding calcium-activated potassium channel - useful in assays
XX to identify compounds which increase or decrease potassium ion flux
XX
PS Claim 3; Page 112; 151pp; English.
XX

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This sequence encodes the human small conductance calcium-activated potassium channel protein 3 (hSK3) of the invention. The proteins of the invention are monomers of a calcium-activated potassium channel, where the monomer: (1) has a calculated molecular weight of between 40 and 80 kDa; and (11) has a calculated molecular weight of between 40 and 80 kDa; and (11) has a unit conductance of between 2 and 60 pS when the monomer is in the functional polymeric form of a potassium chain and is expressed in a *Xenopus* oocyte. Antibodies specific for the protein, and probes specific for the DNA can be used to detect the presence of the protein or DNA sequences in a sample. Host cells expression of the protein can be used in assays to identify compounds which increase or decrease the potassium ion flux through the protein. The transfected host cell can also be used for the recombinant production of the protein. The CC DNA sequences can also be used for determine mutations in the SK and IK genes in a computer system. The proteins encoded by the SK and IK genes can be used in a computer system for determining their three dimensional structure, which is useful for determining ligands that bind to the proteins.

SO Sequence 1674 BP; 392 A; 521 C; 409 G; 352 T; 0 other;

alignment_scores:

Quality:	2125.50	Length:	585
Ratio:	4.209 <td>Gaps:</td> <td>4</td>	Gaps:	4
Percent Similarity:	86.325	Percent Identity:	73.162

alignment_block:

US-09-254-590-19 x V35458 ..

Align seg 1/1 to: V35458 from: 1 to: 1674

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1 ATGAGCTCTCCGCAAGTATAGTGGGTGATGAGGCCCTCAGCCGCT 50
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17 userAlaSerArgArgAsnLeuHisGluMetAspSerGluAlaGlnPro 34
  |||
51 CAGCGCTCTCCGAGAGACCTCATTCGAGCCGAGAGATGAGGAGCAACCC 100
  |||
34 enGlnProProAlaSerValGlyGlyGlyGlyGlyAlaSerProSer 50
  |||
101 TCCAG.....CTTTCCAGCCCT... 117

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1734 GGTACCAAGACACAGAGAGTAACTTTCCTGGTCCATGCG 1783
351 LeuIleSerIleThrPheLeuSerIleGlyrcylAspMetValProAs 367
1784 CTCATCTCATCATCATCTTCTTCATTTGGTTATGGGACATGTCCCA 1833
367 nhrtyrcysgilyysgilyvalcysleuLeuThrGlyIleMetGlyalag 384
1834 CACATACCTGGGAAAGGTCTCTCTCTCCTCAGCTGACATCATGGGTGAG 1883
384 LysThrAlaLeuValAlaValAlaValAlaArgysleuGluLeuThr 400
1884 CCTGCACTGCCCTTGTGGCGCGGTGGCCGCAAGAGCTGACCTACC 1933
401 LysAlaGluLysHisValHisAspMetLeuAspThrGluLeuThrly 417
1934 AAGCGGAGAGAGAGCTTCATTAACCTCATGATGACAGCTCAGCCAA 1983
417 sArgValLysAsnAlaAlaAlaAsnValLeuArgGluThrProLeuIle 434
1984 GCGGATCAAGATGCTCGAGCCATGCTCTCGGAAACATGGTTATCT 2033
434 YLYsAsnThrLysLeuValLysLysylAspHisAlaLysValArglys 450
2034 ATTAACACACAAAGCTGCTTAAGAGATTGACCATGCAAGAGAGGAAA 2083
451 HisGlnArgLysPheLeuGlnAlaIleHisGlnLeuArgSerValLysMe 467
2084 CACGAGAGAGAGAGTCTTCAAGCATTCACACAGTTGAGAGCCTCAAGT 2133
467 tGluGlnArgLysLeuAsnAspGlnAlaAsnThrLeuValAspLeuAla 484
2134 GAAGACAGAGAGAGAGTCTTCAAGCATTCACACAGTTGAGAGCCTTCCA 2183
484 YsrhrcLysAsnLysMetLysAspMetLysAspLeuAsnGluArgSer 500
2184 AGTTCAGAGATCATGTATGATCATACAGAACTCATGACCGAGC 2233
501 GluAspPheGluLysArgIleValThrLeuGluThrLysLeuGluThrLe 517
2234 GAAGACAGAGAGAGAGTCTTCAAGCATTCACACAGTTGAGAGCCTTCCA 2283
517 uileGlySerIleHisAlaLeuProGlyLeuIleSerGlnThrIleArg 534
2284 CACGCCAGCTTCAACTCCCTGCTCTCATGCGGACACCTCGCCG 2333
534 IngGlnArgAspPheIleGluAlaGlnMetGluSerLysPheHis 550
2334 AGCAGACAGAGAGAGTCTTCAAGCATTCACAGAGCGGAGGTGTCAGC 2383
551 ValThrTyraAsnAlaGluArgSerArgSerSerArgArgArgArgse 567
2384 GTGGCAGTGGGACACACCCCAATCTCCGATCCGAGAGCCCATTTGGGGT 2433
567 rSerSerThrAlaProProThrSerSerGluSerSer 579
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seq_documentation_block:
ID V35447 standard: cDNA, 1659 BP.
XX
AC V35447:
XX
DE 01-OCT-1998 (first entry)
XX
DE Rat truncated rSK3 coding sequence.
XX
XX Small conductance calcium-activated potassium channel protein 1:
XX rSK3: rat; potassium ion flux; ss.
OS Rattus sp.

```

```

XX
PN MO9811139-A1.
XX
PD 19-MAR-1998.
XX
PF 10-SEP-1997; 97WO-US16033.
XX
PR 17-APR-1997; 97US-0045233.
PR 11-SEP-1996; 96US-0026451.
PR 07-MAR-1997; 97US-0040052.
XX
PA (ICAG-) ICAGEN INC.
XX (UDOR-) UNIV OREGON HEALTH SCI.
XX
PI Adelman JP, Bond CT, Maylie J, Silvia CP;
DR WPI; 1998-207332/18.
DR P-PSDB; W63703.
XX
PT DNA encoding calcium-activated potassium channel - useful in assays
PT to identify compounds which increase or decrease potassium ion flux
XX
PS Claim 3; Page 105; 151pp; English.
XX

```

This sequence encodes the rat small conductance calcium-activated potassium channel protein 3 (rSK3) of the invention. The proteins of the invention are monomers of a calcium-activated potassium channel, where the monomer: (i) has a calculated molecular weight of between 40 and 80 kDa; and (ii) has a unit conductance of between 2 and 60 pS when the monomer is in the functional polymeric form of a potassium chain and is expressed in a *Xenopus* oocyte. Antibodies specific for the protein, and probes specific for the DNA can be used to detect the presence of the protein or DNA sequences in a sample. Host cells expression of the protein can be used in assays to identify compounds which increase or decrease the potassium ion flux through the protein. The transfected host cell can also be used for the recombinant production of the protein. The DNA sequences can also be used for determine mutations in the SK and IK genes in a computer system. The proteins encoded by the SK and IK genes can be used in a computer system for determining their three dimensional structure, which is useful for determining ligands that bind to the proteins.

Sequence 1659 BP; 404 A; 499 C; 398 G; 358 T; 0 other.

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Ratio: 4.243 Gaps: 5
Percent Similarity: 85.567 Percent Identity: 72.680

alignment_block:
US-09-254-590-19 x V35447 ..

Align seg 1/1 to: V35447 from: 1 to: 1659

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34 eugInProProAlaSerValGlyGlyGlyGlyAlaSerSerProSer 50
101 TCCAG.....CTCTCACTCC... 117
51 AlalaAlaAlaAlaAlaAlaValSerSerSerAlaProGluIleVal 67
118 .....AGCAACCCCGCAGAGATTAT 137
67 lValSerLysProGluHisAsnAsnSerAsnAlaLeuAlaLeuTyrglyT 84
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1108 cggagactcgcaactcacaacagcagagacatgtgcacaaacttcattgat 1157
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1158 ggaactacactcaccnaacgattcaaaagacgtccgcccaatgctctcc 1207
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1208 gggaaacattgctcattgtacaaacacacaaacgtctgtaaagaaattgac 1257
445 hisalalyvalatgltysnhsiglnatgltyspheuenglnalalehsgl 461
1258 caagccaaagtcagaaacaccagagagaattctcccaagctattgcaca 1307
461 pleuatyservallysmetnnglntrptryleuasnprclnalaaspt 478
1308 actgaaggggtgcnaagatggaaacaaagaaagcttgatgaccacaaacca 1357
478 htleuvalaspleuadalystrthrlnasnilemettytasmettleaser 494
1358 ccctgtgacactttccaaagatgcagaaacgcatgtatgactgtattatcc 1407
495 aspleuasngluatyserserghlyasprhegltysargilevalthrleugl 511
1408 gagcttaacagcaacggaaagaaagacgtgaaamaagaaattggcaccstgga 1457
511 thtrlytleugltuthrleuileuglyserllehnsialeuproblyleu 528
1458 atccaaagctggagacscgtcacagccaaacttcattgtccctccctgtca 1507
528 lesergltthrleatrglnnglnatrgasprheileuualaglmets 544
1508 ttcgagacacacccctggccacacagacagacagctgctacgtccctgtgc 1557
545 glusertyrasprlynhisvalthrtyasnaiaiaagltasratargserse 561
1558 gaggccccggggcattcagctgctctgc..... 1584
seq_name: /STD56/gcgdata/geneseq/geneseqn/NA1998.DAT.V35445
seq_documentation_block:
ID: V35445 standard; cDNA; 1683 BP.
XX V35445;
XX AC
XX AT
XX 01-OCT-1998 (first entry)
XX DE
XX Human hSK1 coding sequence.
XX NM
XX Small conductance calcium-activated potassium channel protein 1,
XX hSK1; human; potassium ion flux; ss.
XX OS
XX Homo sapiens.
XX FH
XX Key Location/Qualifiers
XX CDS 1..1683
XX /tag= a
XX /transl_except= (pos:490..492, aa:Ile)
XX /note= "no stop codon given"
XX FT
XX PN W09811139-A1.

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PD 19-MAR-1998.
XX
XX 10-SEP-1997; 97WO-US16033.
XX
XX 17-APR-1997; 97US-0045233.
XX
XX 11-SEP-1996; 96US-0026451.
XX
XX 07-MAR-1997; 97US-0040052.
XX
XX (ICAC-) ICAGEN INC.
XX (UOR-) UNIV OREGON HEALTH SCI.
XX
XX Adelman JP, Bond CT, Maylie J, Silvia CP;
XX WPI; 1998-207332/18.
XX P-PSDB; W63701.
XX
XX DNA encoding calcium-activated potassium channel - useful in assays
XX to identify compounds which increase or decrease potassium ion flux
XX
XX Claim 3; Page 101-102; 151pp; English.
XX
XX This sequence encodes the human small conductance calcium-activated
XX potassium channel protein 1 (hSK1) of the invention. The proteins of the
XX invention are monomers of a calcium-activated potassium channel, where
XX the monomer: (1) has a calculated molecular weight of between 40 and
XX 80 kDa; and (11) has a unit conductance of between 2 and 60 pS when the
XX monomer is in a Xenopus oocyte. Antibodies specific for the protein, and
XX probes specific for the DNA can be used to detect the presence of the
XX protein or DNA sequences in a sample. Host cells expressing or
XX decreasing the potassium ion flux through the protein. The transfected host
XX cell can also be used for the recombinant production of the protein. The
XX DNA sequences can also be used for determining mutations in the SK and IK
XX genes in a computer system. The proteins encoded by the SK and IK genes
XX can be used in a computer system for determining their three dimensional
XX structure, which is useful for determining ligands that bind to the
XX proteins.
XX
XX Sequence 1683 BP; 319 A; 582 C; 502 G; 280 T; 0 other:
XX
XX
XX alignment_scores:
XX      Quality: 1865.50      Length: 538
XX      Ratio: 4.064      Gaps: 7
XX      Percent Similarity: 85.316      Percent Identity: 70.074
XX
XX alignment_block:
XX US-09-254-590-19 x V35445
XX
XX Align seg 1/1 to: V35445 from: 1 to: 1683
XX
XX 1 MetSerSerCysArgTyrAsnGlyValMetArgProLeu...SerAs 16
XX 55 ATGAACAGCCACAGACGATACAGCGCTGCGCGCGCGCGCGCGCGCG 104
XX 16 nLeuSerAlaSerArgTyrAsnGlyValMetArgProLeu...G 32
XX 105 GCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 148
XX 32 InProLeuGlnProProAlaSerValGlyGlyGlyValAlaSerSer 48
XX 149 ACCCGCCACAGCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 183
XX 49 ProSerAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAla 65
XX 184 GTGGTAGTGGCCAGAGTGAAGCCCGCGCGCGCGCGCGCGCGCGCG 233
XX 65 uLeuValAlaSerLysProGluHisAsnAsnSerAsnAsnLeuAla 82
XX 234 G.....GGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 264
XX 82 yrgLylGlyGlyGlySerThrGlyGlyGlyGlyGlyGlyGlyGly 98
XX
XX 264 .....
XX 99 SerGlyHisGlySerSerSerGlyThrLysSerSerLysLysAsnL 115
XX 265 GATGATGAGGAGAGATGAGCGCGCGCGCGCGCGCGCGCGCGCGCG 314
XX 115 nAsnLleGlyTyrLysLeuGlyHisArgAlaAlaLeuPheGlyLys 132
XX 315 AAATGGGGCCAGCCGCTGGCGCGCGCGCGCGCGCGCGCGCGCGCG 364
XX 132 ysaArgLeuSerAspTyrAlaLeuLlePheGlyMetPheGlyIleVal 148
XX 365 AGCGCCCTCAGCGACATGATGCCCTTATTTGGCATGCTTGGCATG 414
XX 149 MetValLleGlyThrGluLeuSerTrpGlyAlaTyrAspLysAla 165
XX 415 ATGGTACGAGACCGAGCTGCTGGGGGGGTACCAAGAGATGCTCT 464
XX 165 uTyrSerLeuAlaLeuLysCysLeuLleSerLeuSerThrLleLeu 182
XX 465 GTACTCATTCGACCTCAATGCTCTGATGAGCTCTCCAGCGCATCTG 514
XX 182 endGlyLeuLleValTyrHisAlaArgGluLleGluLeuPheMet 198
XX 515 TGGGTGCTGTTGCTCTTACCATGCGCGGAGATCCAGCTGTTCATG 564
XX 199 AspAsnGlyAlaAspArgTyrAlaLeuMetThrTyrGluArgLep 215
XX 565 GACAAAGGGGCTGATGATGGCGCATGCCCATGACCTCGGAGCGGT 614
XX 215 ePheLleCysLeuGluLleLeuValCysAlaLleHisProLlePro 232
XX 615 CCTCATTCGCTAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 664
XX 232 snTyrThrPheThrThrAlaArgLeuAlaPheSerTyrAlaPro 248
XX 665 ACTACCGCTTACGTCGAGCGCGCGCGCGCGCGCGCGCGCGCGCG 714
XX 249 ThrThrThrAlaAspValAspLleLleLeuSerLleProMetPhe 265
XX 715 GTGGCGGAGGCCAGCTGAGCGCTGCTGCTGCTGCTGCTGCTGCTG 764
XX 265 gLeuTyrLeuLleAlaArgValMetLeuLeuHisSerLysLeuPhe 282
XX 765 CCTTACCTGCTGGCGCGGATGATGATGATGATGATGATGATGAT 814
XX 282 sPalaSerSerArgSerLleGlyAlaLeuAsnLysLleAsnPheAs 298
XX 815 AGCGCTGAGCGCGAGCATCGCGCGCGCGCGCGCGCGCGCGCGCG 864
XX 299 ArgPheValMetLysThrLeuMetThrLleCysProGlyThrVal 315
XX 865 GCGTTCGCTCATGAAGACATCATCATCATCATCATCATCATCATCAT 914
XX 315 uValPheSerLleSerLeuTrpLleLleAlaIleArgPheValArg 332
XX 915 GGTCTTACGATCTCTCTGAGATCATTCGACCGCTGCGCGGTCT 964
XX 332 ysgLysArgTyrHisAspGlnAspValThrSerAsnPheLeuGlyAla 348
XX 965 GCGAGAGGTACCAAGACAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1014
XX 349 MetTrpLeuLleSerLleThrPheLeuSerLleGlyTyrGlyAsp 365
XX 1015 ATGTGCTGATTTCCATCATCTCTCTCATTTGCTACGCGCATGTGT 1064
XX 365 lProAsnThrTyrCysGlyLysGlyAlaCysLeuLeuThrGlyLle 382
XX 1065 GCGCCAGACCTTACGCGGAGAGAGAGAGAGAGAGAGAGAGAGAG 1114
XX 382 lValAlaCysThrAlaLeuValAlaValAlaValAlaArgLysLeu 398
XX

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457 TTTCTGCGCCTATCTGCTGGCTGGGTCATGCTCTCCACACCCCAT 506
279 uphethrAspalaSerSerArgSerIleGlyAlaLeuAnlysIleasn 296
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296 heantrhrArgPheValMetLysThrLeuMetThrIleCysProGlyThr 312
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313 ValLeuValPheSerIleSerLeuThrIleIleAlaIatPhePhe 329
607 GTGCTGTGTGTCTTCACCATCTCTCTGATGCTGCTGCTGATGACAGT 656
329 LArgAlaCysGluArgTyrHisAspGlnAspValThrSerAsnPhe 346
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707 TGGGGGCGCATGTGGCTCATCTCCATTCCTCTCTGCTCATGCGCTACGG 756
363 AspMetValProAsnThrTyrCysGlyLysGlyAlaCysLeuLeuThr 379
757 GACATGCTGCGCCGACACCTACTGTGGAGGCGCTGTCTGCTCACCGG 806
379 yIleMetGlyAlaGlyCysThrAlaLeuValAlaValAlaValArgL 396
807 CATCATGGAGGAGGAGCTGACCTGCTGCTGCTGCTGCTGCTGCTGCTG 856
396 yLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 412
857 AGTTGGACATCACACAGGCTGAGAAACAGCTGACCACTCATGATGAC 906
413 ThrGlnLeuThrLysArgValLysAsnAlaAlaIleAsnValLeuArg 429
907 ACACAGCTCACCAAGCGGTTAAACCGCGCTGCAACCTCTCTCAGGGA 956
429 uThrTrpLeuIleTyrLysAsnThrLysLeuValLysLysIleAsnHis 446
957 GACATGCTGCTCATCACACAGGCTGAGTGAACAGACAGCCAGCAAA 1006
446 LAlaValArgLysHisGlnArgLysPheLeuGlnAlaIleHisGln 461
1007 GCGGGCTTCGGAAACACAGCCTAAGTCTCTTCAAGCATTCATCAGGCG 1056
462 .....LeuArgSerValLysMetGlnIleArgLysLeuAsnAspGlnAl 476
1057 CAGAAAGCTCGGAGACTGTGAAGATTCACACAGGAGAGTGAATGATCAGC 1106
476 AsnThrLeuValAspLeuAlaLysThrGlnAsnIleMetTyrAspMet 493
1107 CACACAGCTGCTGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1156
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510 LeuGlnThrLysLeuGlnThrLeuIleGlySerIleHisAlaLeuPro 526
1207 CTGGAGAGCCGCTGATGATCTGAGGCGCTCCCTCAGAGCCCTAACAG 1256
526 yLeuIleSerGlnThrIle 532
1257 TCTCATGAGCCACAGCCATA 1275

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seq_documentation_block:

ID X00627 standard; DNA; 1099 BP.

AC X00627;

XX

DT 25-MAR-1999 (first entry)

XX Human secreted protein gene 17 clone HELBA06.

DE Human; secreted protein; fusion protein; gene therapy; protein therapy;

XX diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia;

XX developmental abnormality; foetal deficiency; blood; allergy; renal; ds;

KW Immune system; asthma; lymphocytic disease; brain; hepatic; lymphoma;

KW inflammation; ischemic shock; Alzheimer's disease; restenosis; AIDS;

KW cognitive disorder; schizophrenia; prostate; obesity; osteoclast; thymus;

KW osteoporosis; arthritis; testis; lung; thyroiditis; thyroid; digestion;

XX endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.

OS Homo sapiens.

XX

XX W09842738-A1.

XX

PD 01-OCT-1998.

XX

PF 19-MAR-1998; 98WC-US05311.

XX

PR 30-MAY-1997; 97US-0050937.

PR 21-MAR-1997; 97US-0041276.

PR 21-MAR-1997; 97US-0041277.

PR 21-MAR-1997; 97US-0041281.

PR 30-MAY-1997; 97US-0042344.

PR 30-MAY-1997; 97US-0048069.

PR 30-MAY-1997; 97US-0048094.

PR 30-MAY-1997; 97US-0048095.

PR 30-MAY-1997; 97US-0048096.

PR 30-MAY-1997; 97US-0048099.

PR 30-MAY-1997; 97US-0048131.

PR 30-MAY-1997; 97US-0048135.

PR 30-MAY-1997; 97US-0048154.

PR 30-MAY-1997; 97US-0048160.

PR 30-MAY-1997; 97US-0048186.

PR 30-MAY-1997; 97US-0048187.

PR 30-MAY-1997; 97US-0048188.

PR 30-MAY-1997; 97US-0048350.

PR 30-MAY-1997; 97US-0048351.

PR 30-MAY-1997; 97US-0048352.

PR 30-MAY-1997; 97US-0048355.

XX 05-AUG-1997; 97US-0054804.

XX

PA (HUMA-) HUMAN GENOME SCI INC.

XX

PI Brewster LA, Duan R, Edner R, Ferrie AM, Florence KA;

PI Greene JW, Hu JS, Lafleur DM, Moore PA, NI J, Olsen HS;

PI Rosen CA, Ruben SM, Shi Y, Young P;

XX

DR WPI: 1999-070066/06.

DR P-PSDB; W67823.

XX

PT New isolated human genes and the secreted polypeptides they encode -

PT useful for diagnosis and treatment of e.g. cancers, neurological

PT disorders, immune diseases, inflammation or blood disorders

XX

PS Claim 1; Page 183-184; 385pp; English.

XX

CC This sequence represents a nucleic acid molecule which encodes a secreted

CC human protein. The gene number, and the clone it is derived from, are

CC detailed in the descriptor line. The gene can be used to generate fusion

CC proteins by linking to the gene to a human immunoglobulin Fc portion

CC (e.g. X00602) for increasing the stability of the fused protein as

CC compared to the human protein only.

CC The invention relates to 87 novel genes and their fragments (nucleic acid

CC sequences: X00611-X00724; amino acid sequences W67807-W68004) which

CC are useful for preventing, treating or ameliorating medical conditions

CC e.g. by protein or gene therapy. Also, pathological conditions can be

CC diagnosed by determining the amount of the new polypeptides in a sample

CC or by determining the presence of mutations in the new polynucleotides.

CC Specific uses are described for each of the 87 polynucleotides, based on

CC which tissues they are most highly expressed in (see X00611 for described

Page 15

469 InArg.LysLeuAsnLysProIleAlaSerIleGluValPro-----

30-MAY-1997; 97US-0048350.
30-MAY-1997; 97US-0048351.

30-MAY-1997; 97US-0048351.

PR 30-MAY-1997; 97US-0048352.
 PR 30-MAY-1997; 97US-0048355.
 PR 05-AUG-1997; 97US-0054804.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 XX
 PI Breuer LA, Duan R, Ebner R, Ferrie AM, Florence KA;
 PI Greene JM, Hu JS, Lallier DM, Moore PA, NI J, Olsen HS;
 PI Rosen CA, Ruben SM, Shi Y, Young P;
 XX
 DR WPI: 1999-070066/06.
 P-PSDB: W67899.
 XX
 PT New isolated human genes and the secreted polypeptides they encode -
 PT useful for diagnosis and treatment of e.g. cancers, neurological
 XX disorders, immune diseases, inflammation or blood disorders
 PS
 PS Claim 1; Page 253-254; 385pp; English.
 CC This sequence represents a nucleic acid molecule which encodes a secreted
 CC human protein. The gene number, and the clone it is derived from, are
 CC detailed in the descriptor line. The gene can be used to generate fusion
 CC proteins by linking to the gene to a human immunoglobulin Fc portion
 CC (e.g. X00602) for increasing the stability of the fused protein as
 CC compared to the human protein only.
 CC The invention relates to 87 novel genes and their fragments (nucleic acid
 CC sequences: X00611-X00724; amino acid sequences W67807-W68004) which
 CC are useful for preventing, treating or ameliorating medical conditions
 CC e.g. by protein or gene therapy. Also, pathological conditions can be
 CC diagnosed by determining the amount of the new polypeptides in a sample
 CC or by determining the presence of mutations in the new polynucleotides.
 CC Specific uses are described for each of the 87 polynucleotides, based on
 CC which tissues they are most highly expressed in (see X00611 for described
 CC uses).
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 US-09-254-590-19 x X00703
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 |||||
 3 GATGTGACATCATCTGCTGTATCCCATGTTCTCGCGCTGTACCTCAT 52
 269 eAlaArGVAlMeLeuLeuHisSerLyLeuPheThraSPAlasSerA 286
 |||||
 53 CCGCGAGTCATGCTGTGACAG. AACCTTTACCGATGCTGTCTCC 101
 286 rGSerLleGlyAlaLeuAnLysIleasnPheasnThraPheValMet 302
 |||||
 102 GCAGCATCGGGGCGCTCAACAGATCACTTCAACCGCGCTTGTCA TG 151
 303 LysThraLeuMetThraLleCysProGlyThraValLeuLeuValPheSerI 319
 |||||
 152 AAGACGCTCATGACATCGCGCTGACACTGCTCTGCTGTGTCAACAT 201
 319 eSerLeuThraLleAlaAlaLThrThraValArgAlaCysGLuArg.... 334
 |||||
 202 CTCTCTGTGATCATTTGCTGCGTGCACCGTCTGTGTGAAGTCCG 251
 335 TyrHisAsp 337
 253 AATCACCAGCCAGCGTTCTGCTCATCATCTTCTGCTGTACCAAGAC 301
 338 GlnGlnAspValThrSerAsnPheLeuGlyAlaMetThrLeuIleSerI 354

|||||
 302 CAGCAGACGTAACACTAGTACTTTTGTGGTGCATGTGGCTCATCTCAT 351
 354 eThraPheLeuSerLleGlyTyrrGlyAspMetValIProasnThraTyrrCysG 371
 |||||
 352 CACATTCCTTTCCATTGTTATGGGACAGATGGGCGCCACACATACGTG 401
 371 LysGlyValAlaCysLeuLeuThraGlyLleMetGlyAlaGlyCysThraAla 387
 |||||
 402 GGAAAGGTGTCTGTCTCCCTCACTGGCATCTAGTGCTGCAGCTGTGC 451
 388 LeuValAlaValAlaValAlaArgLysLeuGluLeuThraLysAlaGlu 404
 |||||
 452 CTGTGTGTGCGCTGTGTGCGGAAACCTGGAACCTCACCACAAAGCGGAA 501
 404 shiValHisAsnPhemeLmeLaspThraGlnLeuThraLysArgValLysA 421
 |||||
 502 GCACGTTCATTAANTTCATGATGACACTGCTACGTCACCAAGGATCACA 551
 421 snAlaAlaAlaAsnValLeuArgGluThraThraLleTyrrLysAsnThra 437
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 552 ATGTGTGACCAATGTCTTSGGAAACATGTGTATCTATAACACACA 601
 438 LysLeuValLysLysIleAspHisAlaLysValArgLysHisGlnArg 454
 |||||
 602 AAGTGTAAAGAAAGATTGACCATGCCCAAGTGAAGAA. CACCAGAGAA 650
 454 sPheLeuGlnAlaLleHisGlnLeuArgSerValLysMetGlnArgL 471
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 651 GTTCTTCCCAAG. ATCCACAGTTTGAAGCGCTCAAGATGAACAGAGA 699
 471 LysLeuAsnAspGlnAlaAsnThraLeuValAspLeuAlaLysThraGlnAsn 487
 |||||
 700 AGCTGAGTGACCAAGCCAAACANTCTGTGACCTTTCACCAAGTGCAGAT 749
 488 IleMetTyrrAspMetLleSerAspLeuAsnGlnArgSerGlnAspPheG 504
 |||||
 750 GTCMTGTATGACTTATATCAGACAACTCAATGACCGAGCGAAGACCTGA 799
 504 LysArgGlyLeuValThraLeuGluThraLysLeuGluThraLleIleGlySerI 521
 |||||
 800 GAAGCAGATGTGGCAGCTGTGAGTCAGACATGACATCTCACCGCCACT 849
 521 LeHisAlaLeuProGlyLeuLleSerGlnThraLleArgGlnIndArg 537
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 850 TCACCTCCCTGCGCTGCTCATGCGCCAGACCTGCGCGCAGAGCAG 899
 538 AspPheLleGlyAlaGlnMetGluSerTyrrAspLysValThrTyrrAs 554
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 900 CAGCTCTGTGTGCATCATGAGCGCGGGGTGTGACGCTGACAGTGG 949
 554 nAlaGluArgSerArgSerSerArgArgArgArgArgSerSerSerThra 571
 |||||
 950 CACACCCACACCCCAATCTCCGATACGCCCATTTGGGGTCAAGCTCCACT 999
 571 LaProProThrSerSerGluSerSer 579
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 1000 CTTTCCGACCCCGTACACAAAGTTCA 1025
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 AC X24831;
 XX
 XX 21-JUN-1999 (first entry)
 DE Mouse calcium activated potassium channel Kca4 orthologue cDNA.
 XX Calcium activated potassium channel. Kca4; mouse; leukocyte; ss.
 OS Mus sp.

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XX  Key                               Location/Qualifiers
FH  CDS                               79..1356
FT                                     /*tag= a
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XX  M09903882-A2.
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XX  28-JAN-1999.
XX
XX  13-JUL-1998; 98WO-GB02058.
XX
XX  09-OCT-1997; 97GB-0021366.
XX  15-JUL-1997; 97GB-0014760.
XX
XX  (ZENE ) ZENECA LTD.
XX
XX  Aiyar J, Logsdon NJ;
XX
XX  WPI, 1999-132158/11.
XX  P-PSDB; W98019.
XX
XX  New isolated leukocyte calcium activated potassium channel nucleic
XX  acids - used to develop products for treating e.g. inflammation,
XX  asthma, allergies, graft rejection, proliferative disorders,
XX  neurodegenerative diseases or autoimmune diseases
XX
XX  Example 18; Page 101; 139pp; English.
XX
XX  This polynucleotide encodes the murine orthologue (see W98019)
XX  of a novel human calcium activated potassium channel (CAPC) that
XX  has been designated hKCa4 (see W98017). The polynucleotide was
XX  isolated following a database search using the hKCa4 amino acid
XX  sequence as query, use of an isolated clone to design PCR primers,
XX  and screening of mouse erythrocytic cell line MEL-C88 cDNA.
XX  The invention also provides expression vectors, antisense
XX  molecules, host cells, purified polypeptides and polynucleotides,
XX  antibodies and (ant)agonists of CAPC function. Compounds that
XX  modulate CAPC activity can be used in treating diseases which are
XX  manifested by dysfunctional leukocytes.
XX
XX  Sequence 1381 BP; 254 A; 404 C; 458 G; 265 T; 0 other:

alignment_scores:
      Quality: 898.50      Length: 471
      Ratio: 2.715      Gaps: 8
      Percent Similarity: 70.276      Percent Identity: 41.826

alignment_block:
US-09-254-590-19 x X24831 ..

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110 erLyLyLyLysAsnGlnAsnIleGlyTyrLyLysLeuGlyHisArgAla 126
112 .....CTGAGACGGAGAAAGCC 129
127 LeuPheGlyLysArgLysArgLysSerLysPyrAlaLeuIlePheGlyMe 143
130 CTGCTGAGACGAGAGAGAGGCTGCGCTGGCTGTGCTGCTGCGCG 179
143 tPheGlyIleValAlaMetValIleGlyThrGlyLeuLeuSerTrpGlyAla 160
180 AACTGCATCGAGCTCATGCTTCTGACAGCTGAGATGTTGTTCTCTCG 229

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230 GGTCAAGTGGTGGTGTACCTGCTCGTGGTAAAGTGTATCATCCGCTG 279
177 SerThrIleIleLeuLeuGlyLeuIleIleValTyrHisAlaArgLys 193
280 TCCAGTGTCTCTCTTGTGTATGTTGTGCTTTCATGCCAAGAGAGT 329
193 eGlnLeuPheMetValAspAsnGlyAlaAspArgLysIleAlaMet 210
330 CCAGCTGTTCATGATGACACAGCGGCTCCGGGACTCGCGCGGCTCGA 379
210 hTyrGlyLysArgIlePhePheIleCysLeuGlyLeuValCysAlaIle 226
380 CCCGGGCGAGGTGGCGAGATCTGCTGAGCTGTGGTGGCGGGTGG 429
227 HisProIlePro.....GlyAsnTyrThr 234
430 CACCGGTGCCCCACGAGACCCGCACTGCGCCCTGGCGGGAGAGCCAC 479
234 rPheThr.....TrpThrAlaArgLeuAlaPheSerTyrAlaProSer 249
480 CGACGGGAGACCCCTGGCGGCTTCTCTG..... 507
249 hTThrAlaAspValAspIleIleLeuSerIleProMetPheLeuArg 265
508 .....GCCAAGCGCAGCGTGTCTGCTCCGCGCATGCTCTGCTGCT 549
266 LeuTyrLeuIleAlaArgValMetLeuLeuHisSerLysLeuPheThr 282
550 CTCTACCTGTGGTCCCGCGGGTGTCTGCTGCGCGGGTCTCTCTCA 599
282 PAlaSerSerArgSerIleGlyAlaLeuAsnLysIleAsnPheAsnThr 299
600 CGGCTCTACGCGACATCGCGGCGCTCAACAGTCCGTTCCGCACT 649
299 rGlyPheAlaMetLysThrLeuMetThrIleCysProGlyThrValLeu 315
650 GGTTCGGCCCAAGCTGATCATGACACGACCGGGTCCCTGCTGCTG 699
316 ValPheSerIleSerLeuTyrIleIleAlaIleAlaThrValAlaGly 332
700 GGCCTCAGCTGGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 749
332 sGluArgTyrHisAspGlnGlnAspValThrSerAsnPheLeuGlyAla 349
750 TGAAGG.....CAGGCTGCATGACACGCGGACCTCAGACACACAC 793
349 eTyrIleIleSerIleThrPheLeuSerIleGlyTyrGlyAspMetVal 365
794 TGTGCTGATTCGATTCATCTCTGACCATGCTGATGGAGCTGTGTA 843
366 ProAsnThrTyrCysGlyLysGlyValCysLeuLeuThrGlyIleMet 382
844 CTGCGACACATGTGGGCGACATGTTGCTGCTGCTGCTGCTGCTGCTG 893
382 yAlaGlyCysThrAlaLeuValAlaValAlaValAlaArgLysLeuGly 399
894 GGTCTGCTGACAGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 943
399 eThrLysAlaGlyLysHisValHisAsnPheMetLysPheGlnLeu 415
944 TCACCAAGCGGAGAAACCGTGCACAACTTCATGATGGAATCCATTA 993
416 ThrLysArgValLysAsnAlaAlaAsnValLeuArgGlyIleThrPhe 432
994 GCCAAGAGATGAAGAGTCAAGCGCGGCTCTGCTGCTGCTGCTGCTG 1043
432 uIleTyrLysAsnThrLysLeuValLysLysIleAspHisAlaValAla 449
1044 GTACCTACAGACACT.....CGAAGAGAGACTCCCGGCTCTGCC 1084
449 rGlyHisGlnArgLysPheLeuGlnAlaIleHisGlnLeuArgSerVal 465

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1085 GCAGATCATCAGCCAGATGCTCGCCGATCCACAGTTCCGCCAGGTA 1134
466 LysMetGlnGlnArgLysLeuAsnAspGlnAlaAsnThrLeuValAspLe 482
1135 CGCGTGAACACCGGAGGCTCGGAGACAGTGAATTCATGCTGAGACAT 1184
482 uAlaLysThrGlnAsnIleMetLysAspMetIleSerAspLeuAsnGlu 499
1185 CTCCAAGATGCATGCTCTGCGACCTGCAGCGTGGCTCCTCCTCT 1234
499 rGSerGluAspPheGlnLysArgIleValThrLeuGlnThrLysLeuGlu 515
1235 CGCACCCTGCGCCCTGGAGAGAAATC.....GAC 1263
516 ThrLeuIleGlySerIleHisAlaLeuProGlyLeuIleSerGlnThrI 532
1264 GGTCTGCGAGGAAAGCTGATCCCTGCAGACCTGCTGCGACCTCT 1313
532 eaArgGlnGlnGln 536
1314 GCAGCAACAGCAG 1326

```

seq_name: /SID56/gcdata/geneseq/geneseq/NA1999.DAT.X24825

seq_documentation_block:

ID X24825 standard; cDNA; 2261 BP.

AC X24825;

DT 21-JUN-1999 (first entry)

DE Human calcium activated potassium channel hKCa4 full-length cDNA.

KW Calcium activated potassium channel; hKCa4; human; leukocyte;

KW T cell; T lymphocyte; inflammation; asthma; allergy;

KW graft rejection; proliferative disorder; anaemia;

KW neurodegenerative disease; autoimmune disease; multiple sclerosis;

KW rheumatoid arthritis; diabetes mellitus; multiple sclerosis;

KW myasthenia gravis; systemic lupus erythematosus;

KW Sjogren's syndrome; mixed connective tissue disease;

KW experimental allergic encephalomyelitis; diagnosis; therapy; ss.

OS Homo sapiens.

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XX This polynucleotide, the coding region of which is claimed, encodes
 CC a novel human calcium activated potassium channel (CACP) designated
 CC hKCa4 (see W98017). This full-length cDNA was isolated from a
 CC human lymph node library. The novel gene maps to human chromosome
 CC 19q13.1-13.2. Transcripts are detected in placenta, prostate,
 CC thymus, spleen, colon and many cell lines of haematopoietic origin.
 CC Calmodulin is an interaction partner for hKCa4 and is possibly the
 CC calcium sensor. hKCa4 is expressed at a high level in activated
 CC T cells. The invention also provides expression vectors, antisense
 CC molecules, host cells, purified polypeptides and polynucleotides,
 CC antibodies and (anti)agonists of CACP function. Compounds that
 CC modulate CACP activity can be used in treating diseases which are
 CC manifested by dysfunctional leukocytes such as acute and chronic
 CC inflammation, asthma, allergies, graft rejection, proliferative
 CC disorders, anaemias, neurodegenerative diseases with immunological
 CC components, as well as autoimmune disease including rheumatoid
 CC arthritis, type-1 diabetes mellitus, multiple sclerosis, myasthenia
 CC gravis, systemic lupus erythematosus, Sjogren's syndrome, mixed
 CC connective tissue disease, and experimental allergic
 CC encephalomyelitis. The products can also be used for gene therapy,
 CC detection and diagnosis.

XX Sequence 2261 BP; 446 A; 660 C; 707 G; 446 T; 2 other;

alignment_scores:

Quality: 891.00 Length: 534

Ratio: 2.468 Gaps: 12

Percent Similarity: 67.603 Percent Identity: 38.951

alignment_block:

US-09-254-590-19 x X24825

Align seg 1/1 to: X24825 from: 1 to: 2261

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35 GlnProProAlaSerValGlyGly.....GlyG1 44
179 GAGCTGCTCCCTGACCTGCGGCTCCCTGCTCCCTGCTCCCTGCTCG 228
44 yG1AlaSerSerProSerAlaAlaAlaAlaAlaAlaAlaValSers 61
229 CCCTGACCACTCCCGACAGAGGCGCTGCTGCTGCTGCTGCTGCTG 278
61 erSerAlaProGlnIleValSerLysProGlnHisAsnSer... 76
279 AGTCCAGAGCCAGCAGAGGAGTGCAGCTGCTGCTGCTGCTGCTGCT 328
77 ...AsnAsnLeuAlaLeuTyrGlyGlyGly.....G1 87
329 CCTGTCGCTGCTGCGAGGTGGGAGCCCTGCGCAGAACCTGCTGAGCC 378
87 yG1SerThrGlyGlyGlyGlyGlyGlySer.GlyHisGlySer 103
379 CCAAGACCCCGGGGGCCATGGGCGGGGATGCTGCTGCTGCTGCTG 428
104 SerSerGlyThrLysSerSerLysLysAsnGlnAsnIleGlyTyr 120
428 .....
120 sLeuGlyHisArgArgAlaLeuPheGlnLysArgLysArgLeuSerAsp 137
429 .TTGAGACCGCCGAAAGCGCTGCTGCGAGGAGAGCTCTGCTGCTG 477
137 yAlaLeuIlePheGlyMetPheGlyIleValIleMetValIleGlyThr 153
478 GGGCAGCTGCTGCTGCGAGAGCTGCTGCTGCTGCTGCTGCTGCTG 527
154 GluLeuSerThrGlyAlaTyrAspLysAlaSerLeuTyrSerLeuAla 170
528 GAGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 577
170 uLysCysLeuIleSerLeuSerThrIleIleLeuGlyLeuIleIle 187

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Tue May 15 08:41:18 2001

us-09-254-590-19.ra1

Page 2

IDENTIFICATION METHOD: E (by experiment)
US-08-864-038A-3
Query Match
Best Local Similarity 5.0%; Score 148; DB 3; Length 738;
Matches 36; Conservative 7; Mismatches 19; Indels 20; Gaps 3;
Db 364 FFWAARLAFSTYPSRAEADYDILISIPMLRLILARMLHSLKETDSSRSISGALNKI 443
Oy 295 NFNTRFVMTLMTICPGVILVSVISLMTIAAMTVRACERYHODQDVSNFLGAMWLSTI 354
Db 444 NFNTRFVMTLMTICPGVILVSVISLMTIAAMTVRACERYHODQDVSNFLGAMWLSTI 354
Oy 355 TELSTGYGDMVPNTYCGKGVCLITGIMAGCTALVAVVARKLETAKKHHVHFMDQ 414
Db 504 TELSTGYGDMVPNTYCGKGVCLITGIMAGCTALVAVVARKLETAKKHHVHFMDQ 414
Oy 415 LTRVYNAANAUVLRETWLYIKNKIKYKKIDIAKVRKORFLQAIHOLRSVKMEORLND 474
Db 564 LTRVYNAANAUVLRETWLYIKNKIKYKKIDIAKVRKORFLQAIHOLRSVKMEORLND 474
Oy 475 QANTLVDAKTONMYDMISDNESDEDKRIYVLETKLETILISIALPGILISOTIQ 534
Db 624 QANTLVDAKTONMYDMISDNESDEDKRIYVLETKLETILISIALPGILISOTIQ 534
Oy 535 QORDEIEMOMESYDKHVTYNAERSSRRSSRRSSRNAPTSSSS 579
Db 684 QORDEIEMOMESYDKHVTYNAERSSRRSSRRSSRNAPTSSSS 579
Oy 684 QORDEIEMOMESYDKHVTYNAERSSRRSSRRSSRNAPTSSSS 579

RESULT 2

US-08-864-038A-3
Sequence 3, Application US/08864038A
Patent No. 6001592

GENERAL INFORMATION:

APPLICANT: KUNIO NAKASHIMA et al.
TITLE OF INVENTION: NOVEL POLYPEPTIDE GENE CDNA, VECTOR
TITLE OF INVENTION: CONTAINING SAID CDNA, HOST CELLS TRANSFORMED WITH SAID
TITLE OF INVENTION: VECTOR, POLYPEPTIDE PRODUCED THEREBY, METHOD OF PRODUCING
TITLE OF INVENTION: SAID POLYPEPTIDE, DNA ENCODING SAID POLYPEPTIDE AND ANTIBODY
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: 812-5 HIRANO
STREET: Isehiden
CITY: Tau-city
STATE: Mie-prefecture
COUNTRY: JAPAN
ZIP: 514-01

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.50 inch, 1.44 MB storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: Microsoft Windows 95
SOFTWARE: Word Perfect 6.1

APPLICATION DATA:
APPLICATION NUMBER: US/08/864,038A
FILING DATE: May 28, 1997

PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 8-184459
FILING DATE: 15-July-1996

ATTORNEY/AGENT INFORMATION:
NAME: C. Bruce Hamburg
REGISTRATION NUMBER: 22,389

REFERENCE/DOCKET NUMBER: F-5610
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)986-2340
TELEFAX: (212)986-2340

INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 738

TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:
ORGANISM: pinclada fucata
CELL TYPE: mantle epithelial cell
FEATURE:
NAME/KEY: peptide
LOCATION: from 1 to 738

IDENTIFICATION METHOD: E (by experiment)
US-08-864-038A-3
Query Match
Best Local Similarity 5.0%; Score 148; DB 3; Length 738;
Matches 36; Conservative 7; Mismatches 19; Indels 20; Gaps 3;
Db 41 GGGGAGSSPSAAAAAAYSSAPETIVSK-----PEHNN-----SNNLXGT 84
Oy 610 GGGGAGSSPSAAAAAAYSSAPETIVSK-----PEHNN-----SNNLXGT 84
Db 85 GGGGAGSSPSAAAAAAYSSAPETIVSK-----PEHNN-----SNNLXGT 84
Oy 666 GGGGAGSSPSAAAAAAYSSAPETIVSK-----PEHNN-----SNNLXGT 84

RESULT 3

US-09-135-021-80
Sequence 80, Application US/09135021A
Patent No. 6150104

GENERAL INFORMATION:
APPLICANT: Splawski, Igor
TITLE OF INVENTION: keating, Mark T.
TITLE OF INVENTION: A HOMOLOGOUS MUTATION IN KVLQ1 WHICH CAUSES JERVELL
FILE REFERENCE: 2323-128
CURRENT APPLICATION NUMBER: US/09/135,021A
EARLIER FILING DATE: 1996-08-17
EARLIER APPLICATION NUMBER: 08/874,655
EARLIER FILING DATE: 1997-06-13
EARLIER APPLICATION NUMBER: 60/094,477
NUMBER OF SEQ ID NOS: 80
SOFTWARE: Patent In Ver. 2.0
SEQ ID NO 80
LENGTH: 581
TYPE: PRT
ORGANISM: Homo sapiens
US-09-135-021-80

Query Match
Best Local Similarity 4.2%; Score 125.5; DB 4; Length 581;
Matches 92; Conservative 79; Mismatches 133; Indels 231; Gaps 21;
Oy 205 WRIAMTYRLEFICELIVCAHPICNTYFTWTAARLAFSAAPSTTADYDILISIPML 264
Db 25 WRIAMTYRLEFICELIVCAHPICNTYFTWTAARLAFSAAPSTTADYDILISIPML 264
Oy 265 RYLIARVYMLHSLKETDSSRSISGALNKINFNTR-----FVMTLMTICPGVILV 316
Db 73 RYLIARVYMLHSLKETDSSRSISGALNKINFNTR-----FVMTLMTICPGVILV 316
Oy 317 FSIIS-----LWII-----AAMTVRACERY-HODQDVSNFLG-----C 375
Db 127 FSIIS-----LWII-----AAMTVRACERY-HODQDVSNFLG-----C 375
Oy 348 -----AMWLSTIFSLGYGDMVPNTYCGKGV-----C 375
Db 187 LAENDAVNESGVERGSYADALMVGVTYITIGYDKVPQTGWGKTIASCPVSFAISFA 246
Oy 376 LITGIMAGCTALVAVVARKLETAKKHHVHFMDQTLKRVKANAANVR-----428
Db 247 LITGIMAGCTALVAVVARKLETAKKHHVHFMDQTLKRVKANAANVR-----428
Oy 429 -----ETWLY-----KNTKLVK-----442
Db 289 AENPDSTWKTIRKAPRSHFTLSPSPKPKSVYVKKKKFKLDKNGVTPEKKMLTVPHI 348
Oy 443 -----IDH-----445
Db 349 TCDDPEERLDHFSVDGDSVYKSPPTLLEYSMPHMKRTNSFAEDLDLGGTLLPTPHI 408

us-09-254-590-19.ra1

[illegible]

	RESULT	4	
	US-09-135-021-2		
	Sequence No. 2, Application US/09135021A		
	Patent No. 6150104		
	GENERAL INFORMATION:		
	APPLICANT: SPLANSKI, IGOR		
	INVENTOR: KALING, MARK T.		
	TITLE OF INVENTION: A HOMOZYGOUS MUTATION IN KYLOT1 WHICH CAUSES JERVELL		
	TITLE OF INVENTION: AND LANGE-NIELSEN SYNDROME		
	FILE REFERENCE: 2323-128		
	CURRENT APPLICATION NUMBER: US/09/135,021A		
	CURRENT FILING DATE: 1998-08-17		
	EARLIER APPLICATION NUMBER: 08/874,655		
	EARLIER FILING DATE: 1997-06-13		
	EARLIER APPLICATION NUMBER: 60/094,477		
	EARLIER FILING DATE: 1996-07-25		
	NUMBER OF SEQ ID NOS: 80		
	SOFTWARE: PatentIn Ver. 2.0		
	SEQ ID NO 2		
	LENGTH: 676		
	TYPE: PRT		
	ORGANISM: Homo sapiens		
	US-09-135-021-2		
	Query Match	4.2%	Score 125.5; DB 4; Length 676;
	Best Local Similarity	17.2%; Pred. No. 0.01;	
	Matches	92; Conservative	79; Mismatches 133; Indels 231; Gaps 21;
OY	205 WRIAMRYEPIFCLEILVCAIHPIGNTYTTFARLAFSVPASTTADVDIILSTPMFL	264	
DY	120 WKCVYHFAVFLL--VLVCLIFSVLS--TTEOTALLA-----TGTLFMEIVLVV--FE	167	
DY	265 RLYLIARVMLHSKILFTDASRSISGALKINKFNTR-----FMKRLMTICPTGLLV	316	
DY	168 GREYVVRLLM-----SAGCRKKYVGLMGRLRFARKRPISITIDLIYVASMYLVCSKSGGV	221	
OY	317 FSIS-----LMIT-----AAVTYRACERY-HDOODVTSNFG-	347	
DY	222 FATSAIRGIRFIOLIMLHVDRGGTKRLLGSVPIHQDELITFLYLIGPLIFSSIFYV	281	
OY	348 -----AMWLISTFSLICYGDMPNYCYGKV-----C	375	
DY	282 LAEKDAVNESGRVEFSYADALAMGVVYTVTTIGYGNKPQWVGKTIKIASCFSEVAISFEA	341	
OY	376 LTUNGAGACIALVAVVARKLETFRKAKEHYHNFMMDTOLTFRKAKNAANVLR-----	428	
DY	342 LPAGILLGSG-----FALKYQOKOROKHEN-----ROTIPASLIOTAMRCYA	383	
OY	429 -----ETWLIY-----KMKTKLVKK-----	442	
DY	384 AENDPSSTWKIYIRKAPRSHTLLSPSPPKKSYYVKKKKKFKLDKDNGVYTPGEKMLTVPHI	443	
OY	443 -----IDH-----	503	
DY	444 TDPPERRRIDHSDYGDVSSEVRKSPFLLEVMSPHFRTSPFAEDLDEGETLLTPITHI	503	
OY	446 AVNRKHOKELQALHOLBSYVMEQRKLINDQANTLVDLAKTONIMYMISDLNERSSEDFEK	505	
DY	504 SOLREHHATKVIKRMQ--FYVAKKKFQQCARPKPYDR-----DVIESIQGHMLMAY	554	
OY	506 RIYLTETKITLIGSIHALPGL--ISGITIROOGRDIEAOEMESYDKVHTVYNAER	557	

555 RIKELORRLOSGK---PSLFISVSEKSKDRGSNTIGARLNFVEDKVTOLODR 605

RESULT 5
 US-08-469-318-148
 Sequence 148, Application US/08469318
 Patent No. 6022535
 GENERAL INFORMATION:
 APPLICANT:
 TITLE OF INVENTION: Multivalent IL-3 Hematopoiesis Fusion
 TITLE OF INVENTION: Protein
 NUMBER OF SEQUENCES: 196
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/469,318
 FILING DATE:
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/446,872
 FILING DATE:
 INFORMATION FOR SEQ. ID NO.: 148:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 337 amino acids
 TYPE: amino acid
 STRANDEDNESS:
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-469-318-148

Query Match	4.1%	Score 120.5	DB 3	Length 337
Best Local Similarity	34.6%	Pred. No. 0.01	30	Indels 35
Matches	37	Conservative	5	Mismatches
QY	5 RYNGGV--RPLSNLSARNTLHMDSEAOPL--QPASVGGGGGAGSPSMAAAAAAAY	59		
Db	148 RAGGCVLASHLDSFLEVSRYRLRL--AQPVPPQPPVNGGGSGGGSGGSGEG	106		
QY	60 SSSAPEIVVSKPEHNNSNNLALYGGGGGSGGGGGSGGSGSGG	224		
Db	201 -----GSGGGSGEGGSGGGSGGSGG			

RESULT 6
 US-08-468-609A-148
 : Sequence 148, Application US/08468609A
 : Patent No. 6030812
 :
 : GENERAL INFORMATION:
 : APPLICANT: Abrams, Mark A.
 : APPLICANT: Bauer, S. C.
 : APPLICANT: Braford-Goldberg, Sarah R.
 : APPLICANT: Caparon, Maite H.
 : APPLICANT: Easton, Alan M.
 : APPLICANT: Klein, Barbara K.
 : APPLICANT: McKeearn, John P.
 : APPLICANT: Olin, Peter O.
 : APPLICANT: Palk, Kunnan
 : APPLICANT: Thomas, John W.
 : APPLICANT: TITLE OF INVENTION: Fusion Proteins Comprising Multiply Mutated Inteleukin-3 (IL-3)
 : NUMBER OF SEQUENCES: 197
 :
 : CORRESPONDENCE ADDRESS:
 : ADDRESSEE: Dennis A. Bennett, G.D. Searle & Co.,
 : ADDRESSEE: Corporate Patent Dept.
 : STREET: P. O. Box 5110
 : CITY: Chicago
 : STATE: Illinois
 : COUNTRY: USA
 : ZIP: 60680
 :
 : COMPUTER READABLE FORM:

Tue May 15 08:41:18 2001

us-09-254-590-19.ra1

APPLICANT: Cappello, Joseph
TITLE OF INVENTION: Functional Recombinantly Prepared
TITLE OF INVENTION: Synthetic Protein Polymer
NUMBER OF SEQUENCES: 119
CORRESPONDENCE ADDRESS:
ADDRESSEE: Flehr, Hohnbach, Test, Albritton & Herbert
STREET: Four Embarcadero Center, Suite 3400
CITY: San Francisco
STATE: CA
COUNTRY: US
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/475,411A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/609,716
FILING DATE: 06-NOV-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/269,429
FILING DATE: 09-NOV-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/114,618
FILING DATE: 29-OCT-1987
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 06/927,258
FILING DATE: 04-NOV-1986
ATTORNEY/AGENT INFORMATION:
NAME: Trecartin, Richard F.
REGISTRATION/DOCKET NUMBER: 31,801
REFERENCE/DOCKET NUMBER: A-55186-9/RFT/MTK
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-398-3249
TELEFAX: 415-398-3249
INFORMATION FOR SEQ ID NO: 49:
SEQUENCE CHARACTERISTICS:
LENGTH: 649 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-475-411A-49
Query Match 4.0%; Score 119.5; DB 4; Length 649;
Best Local Similarity 40.0%; Pred. No. 0.032; 33; Indels 1; Gaps 1;
Matches 28; Conservative 8; Mismatches 33; Indels 1; Gaps 1;
OY 38 ASVGCGGAGSSPAAAMAAVSSAPETIVSKPEHNNSNNLLVYGTGGGSGTG-CGGCG 96
DB 49 SGAGAGSGAGAGSGAGAGSGAGAGSGAGALCVSEPGTIGSRCDAGYAGAGSGAGSGAG 108
OY 97 GCGSHGSSSG 106
DB 109 AGSGAGAGSG 118
RESULT 10
US-08-478-029A-49
Sequence 49, Application US/08478029A
Patent No. 6184348
GENERAL INFORMATION:
APPLICANT: Rerrail, Franco A.
TITLE OF INVENTION: Functional Recombinantly Prepared
TITLE OF INVENTION: Synthetic Protein Polymer
NUMBER OF SEQUENCES: 119
CORRESPONDENCE ADDRESS:

ADDRESSEE: Flehr, Hohnbach, Test, Albritton & Herbert
STREET: Four Embarcadero Center, Suite 3400
CITY: San Francisco
STATE: CA
COUNTRY: US
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/478,029A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/609,716
FILING DATE: 06-NOV-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/269,429
FILING DATE: 09-NOV-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/114,618
FILING DATE: 29-OCT-1987
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 06/927,258
FILING DATE: 04-NOV-1986
ATTORNEY/AGENT INFORMATION:
NAME: Trecartin, Richard F.
REGISTRATION/DOCKET NUMBER: 31,801
REFERENCE/DOCKET NUMBER: A-55186-8/RFT/MTK
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-398-3249
TELEFAX: 415-398-3249
INFORMATION FOR SEQ ID NO: 49:
SEQUENCE CHARACTERISTICS:
LENGTH: 649 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-478-029A-49
Query Match 4.0%; Score 119.5; DB 4; Length 649;
Best Local Similarity 40.0%; Pred. No. 0.032; 33; Indels 1; Gaps 1;
Matches 28; Conservative 8; Mismatches 33; Indels 1; Gaps 1;
OY 38 ASVGCGGAGSSPAAAMAAVSSAPETIVSKPEHNNSNNLLVYGTGGGSGTG-CGGCG 96
DB 49 SGAGAGSGAGAGSGAGAGSGAGAGSGAGALCVSEPGTIGSRCDAGYAGAGSGAGSGAG 108
OY 97 GCGSHGSSSG 106
DB 109 AGSGAGAGSG 118
RESULT 11
US-08-469-318-151
Sequence 151, Application US/08469318
Patent No. 6022535
GENERAL INFORMATION:
APPLICANT: Multivariant IL-3 Hematopoiesis Fusion
TITLE OF INVENTION: Protein
TITLE OF INVENTION: Protein
NUMBER OF SEQUENCES: 196
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/469,318

Tue May 15 08:41:18 2001

us-09-254-590-19.ra1

Page 6

FILED DATE:
CLASSIFICATION:
PRIOR APPLICATION:
APPLICATION NUMBER: 08/446,872
FILING DATE:
INFORMATION FOR SEQ ID NO: 151:
SEQUENCE CHARACTERISTICS:
LENGTH: 349 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-469-318-151

Query Match
Best Local Similarity 4.0%; Score 117.5; DB 3; Length 349;
Matches 37; Conservative 5; Mismatches 30; Indels 41; Gaps 4;

QY 5 RYNGVW--RPLNLSASRRNLHMDSEAOPL-----OPPASVGGGGGASSPSMAA 53
DB 148 RRAGVLYASHLOSFLEVSYRVLRLH---AOPYIEGRISPPQPVWAGGSGGSGGSGE 204
QY 54 AAAAIVSSAPEIYVSKPEHNNSNNLALYGTGGGGSTGGGGGGGSGGSSG 106
DB 205 GG-----GSEGGSGSGSGSGSGSGSGSGSG 230

RESULT 12

US-08-468-609A-151
Sequence 151, Application US/08468609A
Patent No. 6030812
GENERAL INFORMATION:
APPLICANT: Adams, Mark A.
APPLICANT: Bauer, S. C.
APPLICANT: Bradford-Goldberg, Sarah R.
APPLICANT: Caparon, Walter H.
APPLICANT: Easton, Alan M.
APPLICANT: Klein, Barbara K.
APPLICANT: McKeown, John P.
APPLICANT: Olin, Peter O.
APPLICANT: Palk, Kuman
TITLE OF INVENTION: Fusion Proteins Comprising Multiply Mutated Inteleukin-3 (IL-3)
NUMBER OF SEQUENCES: 197
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dennis A. Bennett, G.D. Searle & Co.,
STREET: P. O. Box 5110
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60680

COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA: US/08/468,609A
FILING DATE: 06-JUN-1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/192,325
FILING DATE: 14-FEB-1994
ATTORNEY/AGENT INFORMATION:
NAME: Bennett, Dennis A.
REGISTRATION NUMBER: 34,547
REFERENCE/DOCKET NUMBER: C-2790/3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (314)737-6986
TELEFAX: (314)737-6972
INFORMATION FOR SEQ ID NO: 151:

SEQUENCE CHARACTERISTICS:
LENGTH: 349 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-468-609A-151

Query Match
Best Local Similarity 4.0%; Score 117.5; DB 3; Length 349;
Matches 37; Conservative 5; Mismatches 30; Indels 41; Gaps 4;

QY 5 RYNGVW--RPLNLSASRRNLHMDSEAOPL-----OPPASVGGGGGASSPSMAA 53
DB 148 RRAGVLYASHLOSFLEVSYRVLRLH---AOPYIEGRISPPQPVWAGGSGGSGGSGE 204
QY 54 AAAAIVSSAPEIYVSKPEHNNSNNLALYGTGGGGSTGGGGGGGSGGSSG 106
DB 205 GG-----GSEGGSGSGSGSGSGSGSGSGSG 230

RESULT 13

PCT-US95-01185-151
Sequence 151, Application PC/TUS9501185
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: Multivariant IL-3 Hematopoiesis Fusion
NUMBER OF SEQUENCES: 196
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/01185
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/192325
FILING DATE: 14-FEB-1994
INFORMATION FOR SEQ ID NO: 151:
SEQUENCE CHARACTERISTICS:
LENGTH: 349 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US95-01185-151

Query Match
Best Local Similarity 4.0%; Score 117.5; DB 5; Length 349;
Matches 37; Conservative 5; Mismatches 30; Indels 41; Gaps 4;

QY 5 RYNGVW--RPLNLSASRRNLHMDSEAOPL-----OPPASVGGGGGASSPSMAA 53
DB 148 RRAGVLYASHLOSFLEVSYRVLRLH---AOPYIEGRISPPQPVWAGGSGGSGGSGE 204
QY 54 AAAAIVSSAPEIYVSKPEHNNSNNLALYGTGGGGSTGGGGGGGSGGSSG 106
DB 205 GG-----GSEGGSGSGSGSGSGSGSGSGSG 230

RESULT 14

US-08-207-904-15
Sequence 15, Application US/08207904
Patent No. 5477002
GENERAL INFORMATION:
APPLICANT: Tuttle, AnnMarie
APPLICANT: Crossland, Lyle D.
TITLE OF INVENTION: Antigen-Specific cDNA Sequences, Genomic

us-09-254-590-19.raii

TITLE OF INVENTION: DNA Sequences and Recombinant DNA Sequences
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: CIBA-GEIGY Corporation
STREET: 7 Skyline Drive
CITY: Hawthorne
STATE: New York
COUNTRY: USA
ZIP: 10532
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: 05/08/207,904
APPLICATION NUMBER: 05/08/207,904
FILING DATE:
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 05/07/908,242
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Lazar, Steven R.
REGISTRATION NUMBER: 32,618
REFERENCE/DOCKET NUMBER: CGC 1624
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919)341-8615
TELEFAX: (919)341-8669
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 148 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
; JS-08-207-904-15

Query Match	Best Local Similarity	Score	DB 1:	Length	DB 2:
Matches	Conservative	29;	8;	Mismatches	34;
		31.9%;	Pred. No. 0.0091;	Indels	20;
				Gaps	3;
Oy	42 GGGGASPSAAAAAAAYSSAPEIYVSPKPHNNSNNLALVGTG-----GGG 88				
Db	2 GGGGGGGGGYVSGCGENGCCNYPPVPPGPQ-TENPYCMPCGCGVGGGCGSGSGG 60				
Oy	89 STGGGGGGGGSGHSSSGTKSSKKNNNTIGY 119				
Db	61 GGGGGGGGGGGYGSgyG-----ENGNCNY 85				

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      LENGTH: 301 amino acids
      type:    amino acid
      STRANDEDNESS: linear
      TOPOLOGY: linear
      MOLECULE TYPE: protein
US-08-469-318-142

Query Match           3.9%; Score 114; DB 3; Length 301;
Best Local Similarity 30.1%; Pred. No. 0.032; 29; Indels 28; Gaps 2;
Matches 28; Conservative 8; Mismatches 29;

QY   14 LNSTASRNRIHMHDEAQLPPAPSVGGGSGAGSSPSAAAAAAAAVSSNPELVSKRPH 73
      | : : : : : ||| : ||| : : : 
DB   103 LVLTLEAQEQGVYYIEGRISLP-QPVNNAGGSGSGGSGGSEBGS----- 143

QY       74 NNSNNIALVTGTGGGSGTGGGGGGGGSGCHGSSS 106
      | : |||| ||| ||| ||| ||| |||
DB       144 -----GSEGCGSGEGGSGCGSGSGGSGSG 167
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Search completed: May 14, 2001, 18:48:34
Job time: 3386 sec

Tue May 15 08:41:18 2001

us-09-254-590-19.ra1


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95 Glycylglycylserglyhislyseraserglythrlysserly 111
1037 .....AGCAGCACCCCTTCCCAAGGCCAACAA 1065
111 Glylylsarginalasn11eglytryllysleu1yhisargvalleup 128
1066 GCGGAAAACCAAAACATTTGGCTTAACTGGGACACAGAGGCCCTCT 1115
128 heglylsarglysarleuserasptfalaileupheglymetp 144
1116 TTGAAAAGAGAAAGGACTGAGTGCATGCTCTATTTTGGAGTTT 1165
145 Glytylevalmetval11eglythrlyleusertrp1yalaTras 161
1166 GGAATGTGTATGTGTATGAGACGAGCTCTTGGGGTTTGTACTC 1215
161 pLyalaSerleuTySerleuAlaleuysCysleu11eserleuSert 178
1216 AAGGACTCATGTTTCTGGCTTGGCCCTGAATGCCGATCATCTTCCA 1265
178 hrllelleu1leu1leu1leu1leu1leu1leu1leu1leu1leu1 194
1266 CCAATCATCTTTGGGCTGATCATGCTTACACACAGCTGAGTCCAG 1315
195 leuphemetvalaspasn1yalaasprparq1lealemetrhy 211
1316 CTCTTCGTGATGACAAAGAGCGGATGCTGGGAGTACCATGACCTA 1365
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1366 CGAGGCCATCTCTACATTAGCTGAGATCTGTGTACACACCA 1415
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1416 CCAATTCCTGGCGAGTACAACTTCTTGGCGGACCCGCTTCTCC 1465
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1466 TACACACCTCCCGGCGGAGGCGCATGTGACATCATCTCTGATCCC 1515
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1516 CAGTTCTCGCCCTGACCTGATGACCCGAGTATGCTGATACACAA 1565
278 y1leuPheTrhAspAlaSerSerArgser11egly1leu1leu1 294
1566 ACCTCTTACCGATGCCCTCTCCCAACATCGGGCCCTCAACAGATC 1615
295 AsnPhenThrArgPheValMetlyThrleuMetThr1leCysProgl 311
1616 AACCTCAACACCGCTTTTCTCATGMAAGCCTCATACCATCTGCCG 1665
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1666 CACTGTCTGCTGCTGATGATCTCTGATGATCATGCTGCTGCTG 1715
328 hValArgAlaCysgluarq1yhisasp1leu1leu1leu1leu1 344
1716 CCGTCCGCTGTGTGAAGTACATGACACGAGAGCTAACTAGTAAC 1765
345 Pheleu1yalemetrpleu1leu1leu1leu1leu1leu1leu1leu1 361
1766 TTTCTGGGTCATGTGGCTCATCTCATCATCTCTTCTTCAATGGTTA 1815
361 rGLyAspMetValProasnTrhTyCysgllysgly1yaleCysleu1 378
1816 TGGGACATGTGTCCACACATCTGTGGAAGTGTCTGTCTCTCTCA 1865
378 hrgly1leu1leu1leu1leu1leu1leu1leu1leu1leu1leu1 394
1866 CTGCAATCATGCTGCTGACGCTGCTGCTGCTGCTGCTGCTGCTG 1915
395 Arglyleu1leu1leu1leu1leu1leu1leu1leu1leu1leu1 411

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1916 CGAAGCTGGAACCTCACCAAGCGGAGAGACAGCTGATTAATCTCATGT 1965
411 tAspTrhGlnleuTrhlysarq1yvalyllysasn1leu1leu1leu1 428
1966 GGACACTCAGCTTACCAAGGATCAAGATGTGACGAAATGTCTTTC 2015
428 rgluThrTrpleu1leu1leu1leu1leu1leu1leu1leu1leu1 444
2016 GGGAAACATGTATATCTATTAACACACAAAGCTGTAAAGAAATGAC 2065
445 HisAlaLyValArglysh1sGlnArglyspheleu1leu1leu1leu1 461
2066 CATGCCAAAGTACGAAACCCAGAGAGATCTCTCCACAGCTTATCC 2115
461 nleuatrgserVallysmet1leu1leu1leu1leu1leu1leu1leu1 478
2116 GTTGAGAGACCTCAAGATGAGACAGAGACCTGATGAGACCAAGC 2165
478 hrlleuValAsp1leu1leu1leu1leu1leu1leu1leu1leu1 494
2166 CTCTGTGAGCTTCCAGATGACAGATGATCATGATGATGATGATCA 2215
495 Asp1leu1leu1leu1leu1leu1leu1leu1leu1leu1leu1 511
2216 GAAGCTCAATGACGAGACGAGACCTGAGAGAGATGAGAGCTGGA 2265
511 uThrlyleu1leu1leu1leu1leu1leu1leu1leu1leu1leu1 528
2266 GTGCAAGCTGAGAGATCTCCAGCCAGCTTACATCTCTGCTGCTCA 2315
528 leSerGlnTrh1leu1leu1leu1leu1leu1leu1leu1leu1 544
2316 TCGCCGACACCTTCCGCGAGACAGACGCTCTGCTGCTCATCAT 2365
545 GluSerTyAspLysh1sValTrhTyAsnAlaGluArgSerArgSer 561
2366 GAGGCCCGGGGTGACGCTGAGAGAGAGAGAGAGAGAGAGAGAG 2415
561 rSerArgTrhArgArgSerSerTrhAlaProProTrhSerSerGlu 578
2416 CGATGCCCCCATTTGGGTGAGCTTCACTCTTCCGAGCCCGTACAA 2465
578 erSer 579
2466 GTTCA 2470

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seq_name: /cgn2_6/plodata/1/ina/5b_COMB.seq.us-09-115-446-5
seq_documentation_block:
: Sequence 5, Application US/09115446
: Patient No. 6165719
: GENERAL INFORMATION:
: APPLICANT: Chandu, George K.
: APPLICANT: Gargus, Jay J.
: APPLICANT: Gutman, George
: APPLICANT: Fantino, Emanualle
: APPLICANT: Kalman, Katarin
: TITLE OF INVENTION: HKCA3/KCNJ3 SMALL CONDUCTANCE CALCIUM
: TITLE OF INVENTION: ACTIVATED POTASSIUM CHANNEL: A DIAGNOSTIC
: FILE REFERENCE: 07306/014001
: CURRENT APPLICATION NUMBER: US/09/115,446
: EARLIER FILING DATE: 1998-07-14
: EARLIER APPLICATION NUMBER: 60/052,556
: EARLIER FILING DATE: 1997-07-15
: EARLIER APPLICATION NUMBER: 60/070,741
: EARLIER FILING DATE: 1998-01-08
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 5
: LENGTH: 2526
: TYPE: DNA

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ORGANISM: Homo sapiens
US-09-115-446-5

Alignment scores:
Quality: 2070.50 Length: 585
Ratio: 4.149 Gaps: 4
Percent Similarity: 85.299 Percent Identity: 71.795

alignment_block:
US-09-254-590-19 x US-09-115-446-5 ..

Align seg 1/1 to: US-09-115-446-5 from: 1 to: 2526

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1 MetSerCysArgTyrAsnGlyValMetArgProLeuSerAsnLeu 17
|||||
814 ATGAGCTCCTGCAGATAGCGGTGGGTGATGAGAGCCCTCAGCGGCT 863
17 uSerAlaSerArgArgAsnLeuHisGluMetAspSerGluAlaGlnProL 34
|||||
864 CAGCGCTCCCGAGAGACCTCATCGAGCGCGAGCTGAGGCCAACCC 913
34 euGlnProProAlaSerValGlyGlyGlyAlaSerSerProSer 50
|||||
914 TCCAG.....CTTTACAGCCT... 930
51 AlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAla 67
|||||
931 .....AGCAACCCCGGAGAGATCCT 950
67 lValSerLysProGluHisAsnAsnSerAsnAsnLeuAlaLeuTyrGlyT 84
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951 CATCTCCTCCCGAGAGACCAACCATGCCCAACCTGCTCATCACC 1000
84 hrGlyGly.....GlyLysThrGlyGlyGly 94
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95 GlyGlyGlyGlySerGlyHisGlySerSerGlyThrLysSerSerLys 111
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1042 .....AGCAGCACCACTTCCCAACCAACCAACCA 1070
111 sLysLysAsnGlnAsnIleGlyTyrLysLeuGlyHisArgArgAlaLeuP 128
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128 heGluLysArgLysArgLeuSerAspTyrAlaLeuIlePheGlyMetPhe 144
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145 GlyIleValIleMetValIleGluThrGluLeuSerTrpGlyAlaTyrAs 161
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1171 GGAATGTTGTTATGATGATAGAGACCAACCAACCAACCAACCAACCA 1220
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|||||
1221 AAAGGACTCATGTTTGTGTTGCTGAAATGCCATACGATGCTGCTCA 1270
178 hrIleIleLeuLeuGlyLeuIleIleValTyrHisAlaArgGluIleGln 194
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1271 CCATCATCTTTGGCTGATCATCGCTACACACACACCTGAGATCAG 1320
195 LeuPheMetValAspAsnGlyAlaAspAspTrpArgIleAlaMetThrTy 211
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1321 CTCTGCTGATGACACACAGCGGATGACGCGGATGACCATGACCTA 1370
211 rgIuArgIlePhePheIleCysLeuGluIleLeuValCysAlaIleHisP 228
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1371 CGAGCGCATCTCTCATAGCTCGAGATGCTGGTGAACACCAACCAACA 1420
228 roIleProGlyAsnTyrThrPheThrTrpAlaArgLeuAlaPheSer 244
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1421 CCATTCCTGGCGAGTACAAAGTTCTTGGGCGGACGCGTGGCTTCTCC 1470

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245 TyrAlaProSerThrThrAlaAspValAspIleIleLeuSerIlePr 261
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1471 TACACACCCCTCCGGGCGAGGCGGATGAGACATATCTCTATCC 1520
261 omethPheLeuArgLeuTyrLeuIleAlaArgValMetLeuLeuHisSerL 278
|||||
1521 CATGTTCTGCGGCTGACCTGATGATGCGCGAGTATGATGCTACACAGCA 1570
278 yLeuPheThrAspAlaSerSerArgSerIleGlyAlaLeuAsnLysIle 294
|||||
1571 AGCTTCCACCGATGCTGCTCCGACATCGGCGGCTCCACACAGATC 1620
295 AsnPheAsnTrpArgPheValMetLysThrLeuMetThrIleCysProG 311
|||||
1621 AACTTCAACACCCCTTTCATGAAGACGCTCATGACCATCTGCGCTGG 1670
311 yThrValLeuLeuValPheSerIleSerLeuTrpIleIleAlaAlaTrp 328
|||||
1671 CACTGCTGCTGCTGTCAGATCTCTCTGATGATCATTCGCTGCTGA 1720
328 hrValArgAlaCysGluArgTyrHisAspGlnGlnAspValThrSerAsn 344
|||||
1721 CCGTCCGCTGCTGTAAGATACATGACACAGAGACGTAATGATAC 1770
345 PheLeuGlyAlaMetTrpLeuIleSerIleThrPheLeuSerIleGlyTy 361
|||||
1771 TTCTGGGTCATGCTGCTCATCTCATCATCATTCCTTCTGCTGA 1820
361 rgLysPheMetValProAsnThrTyrCysGlyLysGlyValCysLeuLeu 378
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1821 TGGGAGACATGTCGCCACACATATCTGGGAAAGTGTCTGCTCTCA 1870
378 hrGlyIleMetGlyAlaGlyCysThrAlaLeuValAlaValAlaValAla 394
|||||
1871 CTGCGATCATGCTGACGTCGACATGCTGCTGCTGCTGCTGCTGCTG 1920
395 ArgLysLeuGluLeuThrLysAlaGluLysHisValHisAsnPheMet 411
|||||
1921 CGAAGCTGGAACCTCCAAAGCGAGAGAGAGAGAGAGAGAGAGAGAG 1970
411 AspThrGlnLeuThrLysArgValLysAsnAlaAlaAlaAsnValLeu 428
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1971 GGAACATCAGCTCACCAGAGATCAAGATGCTGACCAATCTCTCC 2020
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seq_documentation_block:
; Sequence 1, Application US/09198839
; Patent No. 6190908
; GENERAL INFORMATION:
; APPLICANT: Kang, Angray S.
; TITLE OF INVENTION: MODULATION OF POLYPEPTIDE DISPLAY ON MODIFIED
; FILE REFERENCE: SCR21115
; CURRENT APPLICATION NUMBER: US/09/198,839
; PRIOR FILING DATE: 1998-12-24
; PRIOR APPLICATION NUMBER: PCT/US99/18207
; PRIOR FILING DATE: 1999-08-11
; PRIOR APPLICATION NUMBER: 60/096,326
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 7083
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: a modified
; US-09-198-839-1

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Ratio: 0.743 Gaps: 21
Percent Similarity: 46.224 Percent Identity: 24.256

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Tue May 15 08:41:22 2001

us-09-254-590-19.rn1

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seq_documentation_block:
Sequence 1, Application US/08440787A
Patent No. 5770434
GENERAL INFORMATION:
APPLICANT: Huse, William D.
TITLE OF INVENTION: Soluble Peptides Having Constrained,
TITLE OF INVENTION: Secondary Conformation in Solution and Method of Making
NUMBER OF SEQUENCES: 174
CORRESPONDENCE ADDRESS:
ADDRESS: Campbell & Flores LLP
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: USA
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/440,787A
FILING DATE: 15-MAY-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/978,893
FILING DATE: 10-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
TELECOMMUNICATION INFORMATION:
REFERENCE/DOCKET NUMBER: P-IX 1586
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 7294 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: circular
US-08-440-787A-1

alignment_scores:
Quality: 150.00 Length: 437
Ratio: 0.743 Gaps: 21
Percent Similarity: 46.224 Percent Identity: 24.256

alignment_block:
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us-09-254-590-19.rn1

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: Patent No. 5770434
: GENERAL INFORMATION:
: APPLICANT: Huse, William D.
: TITLE OF INVENTION: Soluble Peptides Having Constrained,
: TITLE OF INVENTION: Secondary Conformation in Solution and Method of Making
: NUMBER OF SEQUENCES: 174
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Campbell & Flores LLP
: STREET: 4370 La Jolla Village Drive, Suite 700
: CITY: San Diego
: STATE: California
: COUNTRY: USA
: ZIP: 92122
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: OPERATING SYSTEM: IBM PC compatible
: SOFTWARE: Patent Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/440,787A
: FILING DATE: 15-MAY-1995
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/978,893
: FILING DATE: 10-NOV-1992
: ATTORNEY/AGENT INFORMATION:
: NAME: Campbell, Kathryn A.
: REGISTRATION NUMBER: 31,815
: REFERENCE/DOCKET NUMBER: P-IX 1586
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (619) 535-8949
: TELEFAX: (619) 535-8949
: INFORMATION FOR SEQ ID NO: 5:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 7294 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: both
: TOPOLOGY: circular
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US-08-440-787A-5

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Ratio:	0.743	Gaps:	21
Percent Similarity:	46.224	Percent Identity:	24.256

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: Sequence 1, Application PC/TUS9107141
: GENERAL INFORMATION:
: APPLICANT: Huse, William D.
: TITLE OF INVENTION: SURFACE EXPRESSION LIBRARIES OF
: TITLE OF INVENTION: RANDOMIZED PEPTIDES
: NUMBER OF SEQUENCES: 61
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Pretty, Schroeder, Brueggemann & Clark
: STREET: 444 South Flower Street, Suite 2000
: CITY: Los Angeles
: STATE: California
: COUNTRY: United States
: ZIP: 90071
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: PCT/US91/07141
: FILING DATE: 19910927
: CLASSIFICATION: 435

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: ATTORNEY/AGENT INFORMATION:
: NAME: Campbell, Cathryn A
: REGISTRATION NUMBER: 31,815
: REFERENCE/DOCKET NUMBER: P31 9072
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (619) 535-9001
: TELEFAX: (619) 535-8949
: INFORMATION FOR SEQ ID NO: 1:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 7294 base pairs
: TYPE: NUCLEIC ACID
: STRANDEDNESS: both
: TOPOLOGY: circular
: PCT-US91-07141-1

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  quality: 150.00      length: 437
  ratio: 0.743         gaps: 21
Percent Similarity: 46.224      Percent Identity: 24.256

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Page 8

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2 STATE: California
3 COUNTRY: United States
4 ZIP: 90071
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6 COMPUTER READABLE FORM:
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8 MEDIUM TYPE: Floppy disk
9 COMPUTER: IBM PC compatible
10 OPERATING SYSTEM: PC-DOS/MS-DOS
11 SOFTWARE: Patent Release #1.0, Version #1.25
12 CURRENT APPLICATION DATA:
13 APPLICATION NUMBER: PCT/US91/07141
14 FILING DATE: 19910927
15 CLASSIFICATION: 435
16
17 ATTORNEY/AGENT INFORMATION:
18 NAME: Campbell, Cathryn A
19 REGISTRATION NUMBER: 31,815
20 REFERENCE/DOCKET NUMBER: P31 9072
21 TELECOMMUNICATION INFORMATION:
22 TELEPHONE: (619) 535-9001
23 TELEFAX: (619) 535-8949
24 INFORMATION FOR SRO ID NO: 5:
25 SEQUENCE CHARACTERISTICS:
26 LENGTH: 7294 base pairs
27 TYPE: NUCLEIC ACID
28 STRANDEDNESS: both
29 TOPOLOGY: circular
30
31 DCT-US91-07141-5

[illegible]


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seq_documentation_block:
; Sequence 2, Application US/08349131
; Patent No. 5871974
; GENERAL INFORMATION:
; APPLICANT: HUSE, WILLIAM D.
; TITLE OF INVENTION: SURFACE EXPRESSION LIBRARIES OF
; NUMBER OF SEQUENCES: 75
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PRETTY, SCHROEDER, BRUEGGEMANN & CLARK
; STREET: 444 SO. FLOWER STREET, SUITE 200
; CITY: LOS ANGELES
; STATE: CALIFORNIA
; COUNTRY: UNITED STATES
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/349,131
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/120,648
; FILING DATE:
; APPLICATION NUMBER: US/07/767,136
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: CAMPBELL, CATHERIN A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P31 8882
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-535-8949
; TELEFAX: 619-535-9001
; INFORMATION FOR SEQ. ID NO. 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7317 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: circular
US-08-349-131-2

alignment_scores:
Quality: 150.00 Length: 437
Ratio: 0.743 Gaps: 21
Percent Similarity: 46.224 Percent Identity: 24.256

alignment_block:
US-09-254-590-19 x US-08-349-131-2
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2779 TTCTCT.....TTTATATGTTCACCTTATATGATGATGAT 2813
226 IleHisProIleProGlyAsnTyrThrPheThrTyrThrAlaArgLeuAl 242
2814 TTC.....TACGTTTGTCTACATCTACTCCGTAATTAAGG 2845
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2846 AGCTTAATCATGCCA.....GTTCTTTGG 2871
259 eIlePheMetPheLeuArgLeu..... 266
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267 ...TyrLeu.....IleAlaArgVa 272
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3199 .....GCTGTTATTTTGTAACTGCAAAATTAAGCTGTGGAAGACG 3240
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seq_documentation_block:
; Sequence 2, Application US/08470297A
; Patent No. 6027933
; GENERAL INFORMATION:
; APPLICANT: HUSE, WILLIAM D.
; TITLE OF INVENTION: SURFACE EXPRESSION LIBRARIES OF
; TITLE OF INVENTION: HETEROMERIC RECEPTORS
; NUMBER OF SEQUENCES: 76
; CORRESPONDENCE ADDRESS:
; ADDRESS: CAMPBELL & FLORES LLP
; STREET: 4370 LA JOLLA VILLAGE DRIVE, SUITE 700
; CITY: SAN DIEGO
; STATE: CALIFORNIA
; COUNTRY: UNITED STATES
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/470,297A
; FILING DATE: June 5, 1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: CAMPBELL, CATHERIN A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-IX 1611
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-535-9001
; TELEFAX: 619-535-8949
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7317 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: circular

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Page 12

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seq_documentation_block:
? Sequence 2, Application PC/TUS9107149
? GENERAL INFORMATION:
? APPLICANT: HUSB, WILLIAM D.
? TITLE OF INVENTION: SURFACE EXPRESSION LIBRARIES OF
? TITLE OF INVENTION: HETEROMERIC RECEPTORS
? NUMBER OF SEQUENCES: 75
? CORRESPONDENCE ADDRESS:
? ADDRESSEE: PRETTY, SCHROEDER, BRUGGEMANN & CLARK
? STREET: 444 SO. FLOWER STREET, SUITE 200
? CITY: LOS ANGELES
? STATE: CALIFORNIA
? COUNTRY: UNITED STATES
? ZIP: 90071
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Floppy disk
? COMPUTER: IBM PC compatible
? OPERATING SYSTEM: PC-DOS/MS-DOS
? SOFTWARE: Piletrin Release #1.0, Version #1.25
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: PCT/US91/07149
? FILING DATE: 19910927
? CLASSIFICATION: 435

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Tue May 15 08:41:22 2001

us-09-254-590-19.in1

Page 13

ATTORNEY/AGENT INFORMATION:
NAME: CAMPBELL, CATHERIN A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P31 8882
TELEPHONE: 619-535-9001
TELEFAX: 619-535-8949
INFORMATION FOR SPO. ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 7317 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: both
TOPOLOGY: circular
PCT-US91-07149-2

Alignment scores: Length: 437
Quality: 150.00 Gaps: 21
Ratio: 0.743
Percent Similarity: 46.224 Percent Identity: 24.256

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seq_documentation_block:
Sequence 4, Application US/08440787A
Patent No. 5770434
GENERAL INFORMATION:
APPLICANT: Huse, William D.
TITLE OF INVENTION: Soluble Peptides Having Constrained,
TITLE OF INVENTION: Secondary Conformation in Solution and Method of Making
TITLE OF INVENTION: Same.
NUMBER OF SEQUENCES: 174
CORRESPONDENCE ADDRESS:

Tue May 15 08:41:22 2001

us-09-254-590-19.in1

Page 14

ADDRESSEE: Campbell & Flores LLP
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: USA
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/440,787A
FILING DATE: 15-MAY-1995
CLASSIFICATION: 435
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 07/978,893
FILING DATE: 10-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
TELEPHONE: (619) 535-9001
TELECOMMUNICATION INFORMATION:
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 7409 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: circular
US-08-440-787A-4

alignment scores:
Quality: 150.00 Length: 437
Ratio: 0.743 Gaps: 21
Percent Similarity: 46.224 Percent Identity: 24.256

alignment block:
US-09-254-590-19 x US-08-440-787A-4 ..

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Sequence 3, Application US/08440787A
Patent No. 5770434
GENERAL INFORMATION:
APPLICANT: Huse, William D.
TITLE OF INVENTION: Soluble Peptides Having Constrained.
TITLE OF INVENTION: Secondary Conformation In Solution and Method of Making
NUMBER OF INVENTIONS: Same.
NUMBER OF SEQUENCES: 174
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell & Flores LLP
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: USA
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/440,787A
FILING DATE: 15-MAY-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/978,893
FILING DATE: 10-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-IX 1586
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
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INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 7445 base pairs

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;
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: circular
US-08-440-787A-3

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alignment_scores:
Quality: 150.00 Length: 437
Ratio: 0.743 Gaps: 21
Percent Similarity: 46.224 Percent Identity: 24.256
alignment_block:
US-09-254-590-19 x US-08-440-787A-3

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Align seg 1/1 to: US-08-440-787A-3 from: 1 to: 7445

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35 GlnProAlaSerValGlyGlyGlyGlyAlaSerSerProSerAl 51
2266 CAACTCTCTGCAATGCTGGCGGCGGCTGCTGCTGCTGCTGCTGCGG 2315
51 aAlaAlaAlaAlaAlaAlaAlaValSerSerSerAlaProGluIleVal 68
2316 CTCGAGGCGTGT..... 2328
68 alSerIyProGluHisAsnSerAsnAsnLeuAlaLeuTyrGlyThr 84
2329 .....GGCTCT 2334
85 GlyGlyGlyGlySerThrGlyGlyGlyGlyGlyGlyGlySerGlyH 101
2335 GAGGTCGCGGTCGAGGTCGCGGCTGCGAGGAGCGGCTCCGCTG 2384
101 sGlySerSerSerGlyThr..LysSerSerLysLysAsnGlnAsn 117
2385 TGCTCTGCTGCTCGGATTTGATTAAGAAAGTGCAGCAAGCTAATA 2434
117 leGly.....TyrLysLeuGlyHisArgArgAlaLeuPheGluLysArg 131
2435 AGGGGCTATGACCGAAATGCCATGAACCGCTCACTGACGCT 2484
132 Lys...ArgLeuSerAspTyrAlaLeuIlePheGly.MethGlyLys 147
2485 AAAGCAAACTGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2534
147 alValMetValIleGluThrGlnLeuSerTrpGlyAlaTyrAspLysAla 163
2535 TTTCATTGTCGACGTTCCGCGCTTCTATGATGATGCTACTGCTG 2584
164 SerLeuTyrSerLeuAlaLeuLysCysLeuIleSerLeuSerThrIle 180
2585 ATTTGCTGCTCTAATTCCTCAATGCTCAAGTCGTCGAGGATTAAT 2634
180 e..... 180
2635 TCACCTTAATGAATATTCCTCAATATTTACTTCCCTCCCTCAATC 2684
181 .....LeuLeuGlyLeuIleLeuAlaTyrHisAlaArgLys 192
2685 GGTGAATGCGCCCTTTGCTTTAGCGCTGTAACCATATGAT... 2731
193 IleGlnLeuPheMetVal.AspAsnGlyAlaAspAspTrpArgIleAla 209
2732 ...TTTCATTGATTTGACAAATAAATTAATTCCTGCTGCTGCTGCTG 2778
209 ethrTyrGluArgIlePhePheIleCysLeuGluIleLeuValCysAla 225
2779 TTTCCT.....TTTATATGTCGACCTTATGATGATTT 2813
226 IleHisProIleProGlyAsnTyrThrPheThrTrpThrAlaArgLeuAl 242
2814 TTC.....TACGTTGCTAATCAGCGCTAATAGG 2845
242 apheSerTyrAlaProSerThrThrAlaAspValAspIleIleLeuS 259

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2846 AGCTTAAATCATGCCA.....GTTCTTTTG 2871
259 erlleProwerPheleuAArgLeu..... 266
2872 GTATTCCGTTATTATTCGTTTCCGTTTCCTTCGTACTTTGTC 2921
267 ...TyrLeu.....IleAlaArgVa 272
2922 GGCATATCTGCTTACTTTCTTAAAGGCTTCGGTAAGATGACTATTGC 2971
272 lMetleuuhHisSerLysleuPheThrAspAlaSerArgSerileG 289
2972 TATTTCATTGTTCTTCCTTATATTCGCTTAAGCTTAACCTCAATTCCTGTCG 3021
289 lValAlaLeuAsnLysIleAsn.....PheAsnThrArgPheValMetLys 303
3022 GTTATCTCTCGATATTACGCGCTCAATTACCTCTGACTTGT...CAG 3068
304 ThrleuMetThrIleCysProGlyThrValleuLeuValPheSerileSe 320
3069 GGTGTTTCAGTTAAATCTCCCGCTAATGCCGCTTCCTGTTTATGTTAT 3118
320 rLeuThrIleIleAlaAla..TrpThrValArgAlaCysGlnArgTyrHis 336
3119 TCTCTGTGTAAAGCGCTGATTTTTCATTTTGACGTTAAACAA..... 3162
337 AspGlnGlnAspValThrSerAsnPheLeuGlyAlaMetTrpLeuIleSe 353
3163 .....AAATCGTTTCTT.....ATTGCG..... 3180
353 rIleThrPheLeuSerileGlyTyrGlyAspMetValProAsnThrTyrC 370
3181 .....ATTGGGATAAATAATATATG..... 3198
370 ysgLyLysGlyValCysLeuLeuThrGlyIleMetGlyAlaGlyCysThr 386
3199 .....GCTGTTATTATTTGTAACTGGCAAAATAGCGCTGCAAAAGACG 3240
387 AlaLeuValValAlaValAlaValAlaArgLysLeuGluLeuThrLysAlaG1 403
3241 CTCGTAGCGGTGGTGAAGATTCAAGATAAAATTT..... 3273
403 uLysHisValHisAsnPheMetMetValAspThrGlnLeuThrLysArgValL 420
3274 .....GTAGCTGGGTGCAAAATAGCAACTAATCTTGATTTAAGGCTTC 3316
420 ysaAsn 421
3317 AAAAC 3321
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